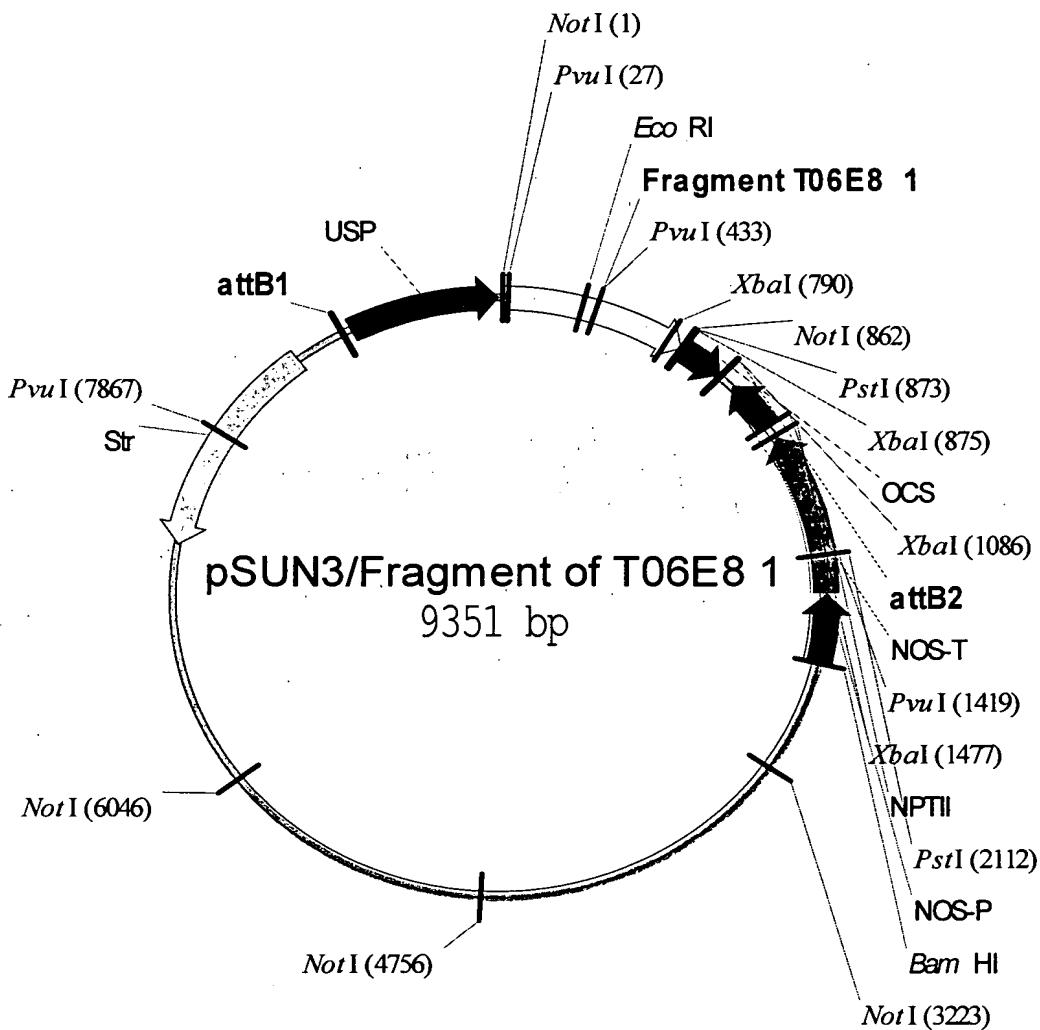


Figure 1: Vector map of pSUN3CeLPLAT



BEST AVAILABLE COPY

Figure 2: Amino acid sequence alignment of *C. elegans* LPLATs (Ce-T06E8.1 and Ce-F59F4.4) with the *M. musculus* LPAAT (Mm-NP061350).

	1	50
Mm-NP061350	MELWPGAWTA LLLLLL <del>L</del> IS TLWFCSSSAK <del>Y</del> E <del>F</del> KMAEYNG <del>W</del> E <del>F</del> FLAILAI	
Ce-T06E8.1	...MENFWSI VVFFLESILF ILYNISTVCH <del>Y</del> YMRISEYYF T <del>I</del> LLHGMEVC	
Ce-F59F4.4	.....MTF LAILFVI <del>A</del> VL LLLAQLPVIG <del>E</del> YI <del>R</del> AVYEGM C <del>L</del> LI <del>G</del> GGFLGG	
	51	100
Mm-NP061350	PVCAVRGRNV ENMKI <del>T</del> RLLL LHAKYLYG <del>T</del> R VEV <del>R</del> GAHHFP PTQ <del>P</del> Y <del>V</del> V <del>S</del> N	
Ce-T06E8.1	VTMIPS <del>W</del> LNG KGADYMFHSF FYWCKWTGVH TT <del>V</del> YGYEK <del>T</del> Q VEGPAV <del>V</del> ICN	
Ce-F59F4.4	LASIPFGKSP NNHFRM <del>F</del> KIF QAMTWP <del>M</del> GV <del>R</del> FE <del>I</del> RNSEILH DKK <del>P</del> Y <del>T</del> IAN	
	101	150
Mm-NP061350	HQS <del>S</del> LD <del>I</del> LLGM MEVLP <del>D</del> RCVP IAKRELL <del>W</del> AG SAGLAC <del>W</del> LAG <del>T</del> P <del>E</del> EDR <del>K</del> R <del>T</del> G	
Ce-T06E8.1	HQS <del>S</del> LD <del>I</del> LSM ASIWP <del>K</del> NCVV MMKRIL <del>A</del> VP FFNLGAYFSN <del>T</del> ED <del>E</del> DRY <del>N</del> RE	
Ce-F59F4.4	HQS <del>A</del> LD <del>V</del> LG <del>M</del> SFAWP <del>V</del> DCVV MLKSSLK <del>Y</del> LP GFNLCA <del>Y</del> LCD <del>S</del> V <del>M</del> INRFSKE	
	151	200
Mm-NP061350	DA <del>I</del> S <del>V</del> M <del>S</del> EVA Q <del>T</del> ELTQDV <del>R</del> W <del>V</del> E <del>P</del> EGTR <del>N</del> H NG <del>S</del> M <del>I</del> P <del>F</del> K <del>R</del> A <del>F</del> H <del>I</del> A <del>V</del> Q <del>A</del> Q <del>V</del>	
Ce-T06E8.1	RAMAS <del>V</del> DYCA SEM <del>K</del> NRNL <del>K</del> W <del>V</del> E <del>P</del> EGTR <del>N</del> R EG <del>G</del> F <del>I</del> P <del>F</del> K <del>K</del> A <del>F</del> N <del>H</del> A <del>V</del> R <del>A</del> Q <del>I</del>	
Ce-F59F4.4	KALKT <del>V</del> DT <del>T</del> TL HE <del>I</del> VT <del>K</del> K <del>R</del> K <del>V</del> W <del>H</del> Y <del>P</del> EGTR <del>N</del> A EPEL <del>E</del> P <del>F</del> K <del>K</del> A <del>F</del> I <del>L</del> A <del>K</del> Q <del>A</del> K <del>I</del>	
	201	250
Mm-NP061350	P <del>I</del> P <del>I</del> IVM <del>S</del> SY Q <del>D</del> F <del>Y</del> SK <del>K</del> ER <del>R</del> FTSP <del>G</del> R <del>C</del> Q <del>V</del> R V <del>L</del> PP <del>V</del> ST <del>E</del> GL TP <del>D</del> D <del>V</del> PA <del>L</del> AD	
Ce-T06E8.1	P <del>I</del> P <del>I</del> P <del>V</del> V <del>F</del> SDY R <del>D</del> F <del>Y</del> SK <del>P</del> GR <del>Y</del> FKNDGEV <del>V</del> IR V <del>L</del> DA <del>I</del> P <del>T</del> K <del>G</del> L TL <del>D</del> D <del>V</del> SE <del>L</del> SD	
Ce-F59F4.4	P <del>I</del> V <del>P</del> CVF <del>S</del> SH K <del>F</del> F <del>Y</del> SHAE <del>K</del> R LTS.GNCI <del>I</del> D IL <del>P</del> EV <del>D</del> SS.. K <del>F</del> DS <del>I</del> DD <del>L</del> SA	
	251	285
Mm-NP061350	SVRHS <del>M</del> LT <del>I</del> F RE <del>I</del> STDGLGG GDCLKKPGGA GEARL	
Ce-T06E8.1	MCRDVMLAAY KE <del>V</del> TLEAQQR NATRRGETKD GKKSE	
Ce-F59F4.4	HCRKIMQAHR EK <del>I</del> DAEAANL NI.....	

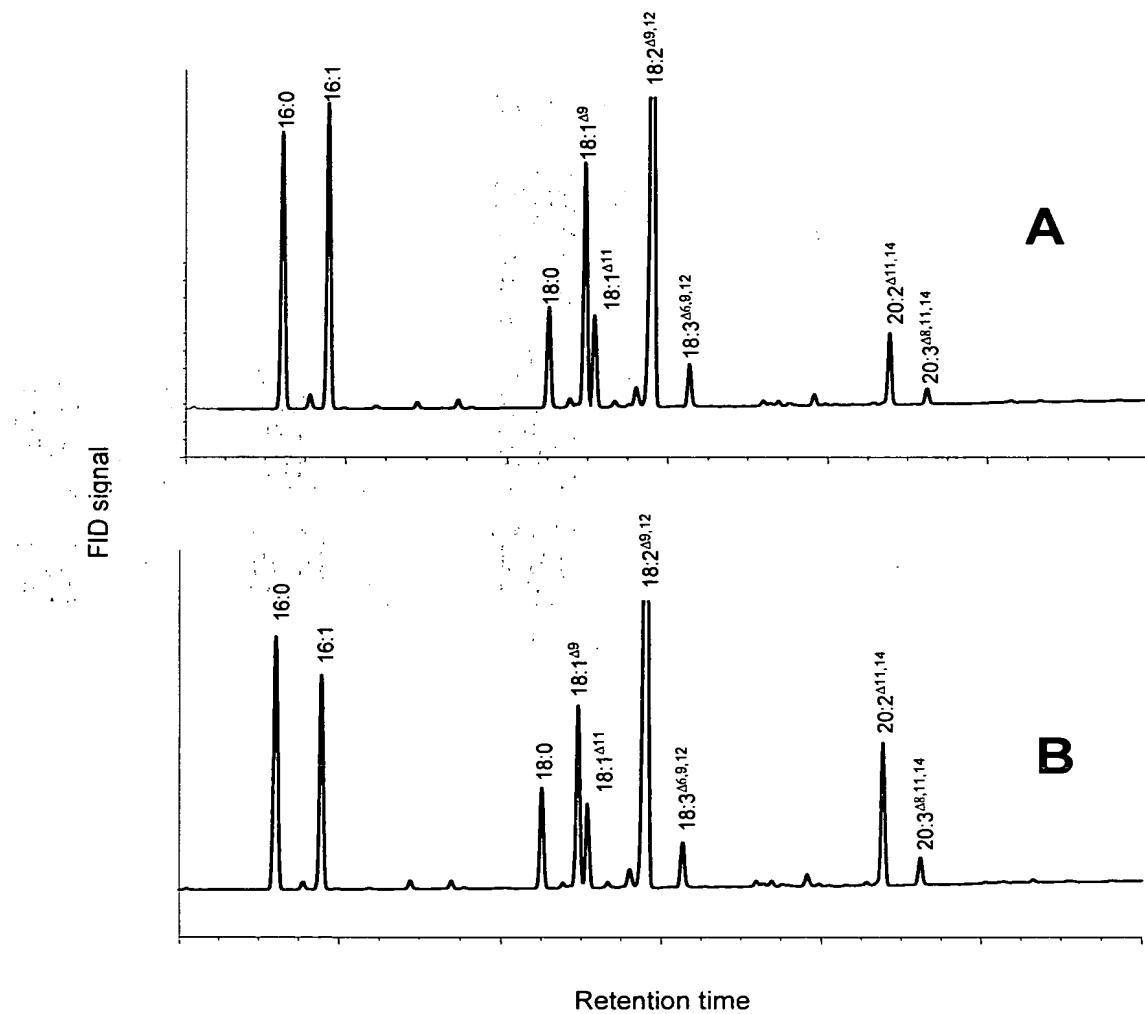
Figure 3: Fatty acid profiles of transgenic C13ABYS86 *S. cerevisiae* cells

Figure 4: Elongation of exogenously applied  $18:2^{\Delta 9,12}$  and  $18:3^{\Delta 9,12,15}$ , respectively, following their endogenous  $\Delta 6$ -desaturation (data from figs 2 and 3).

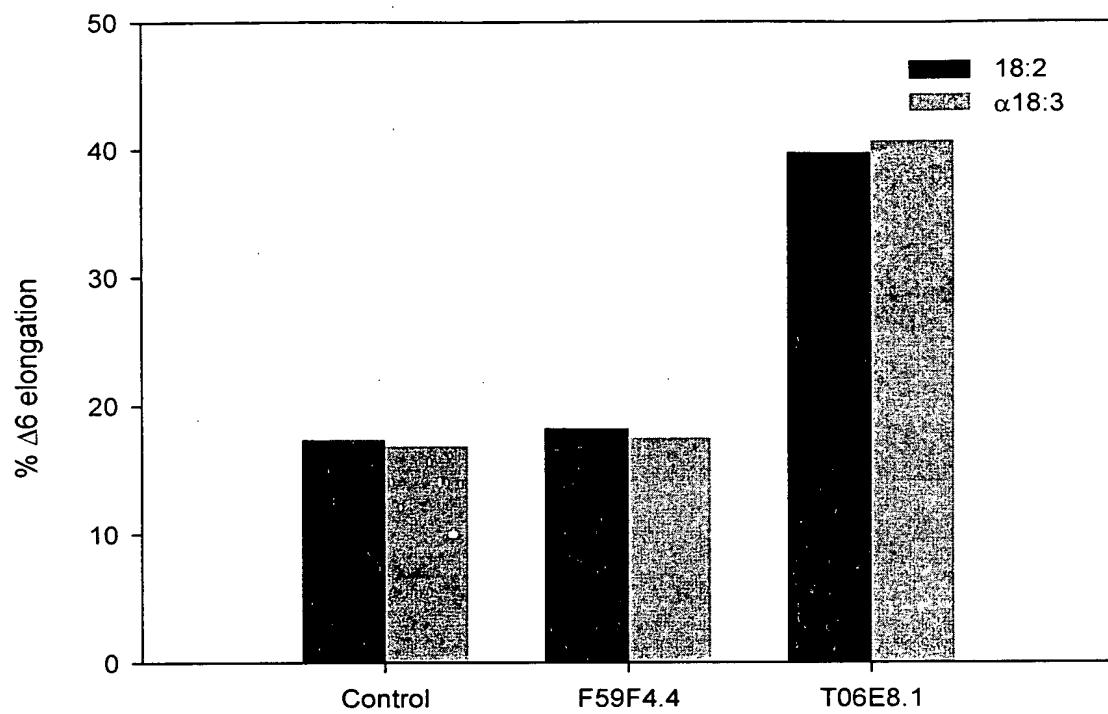


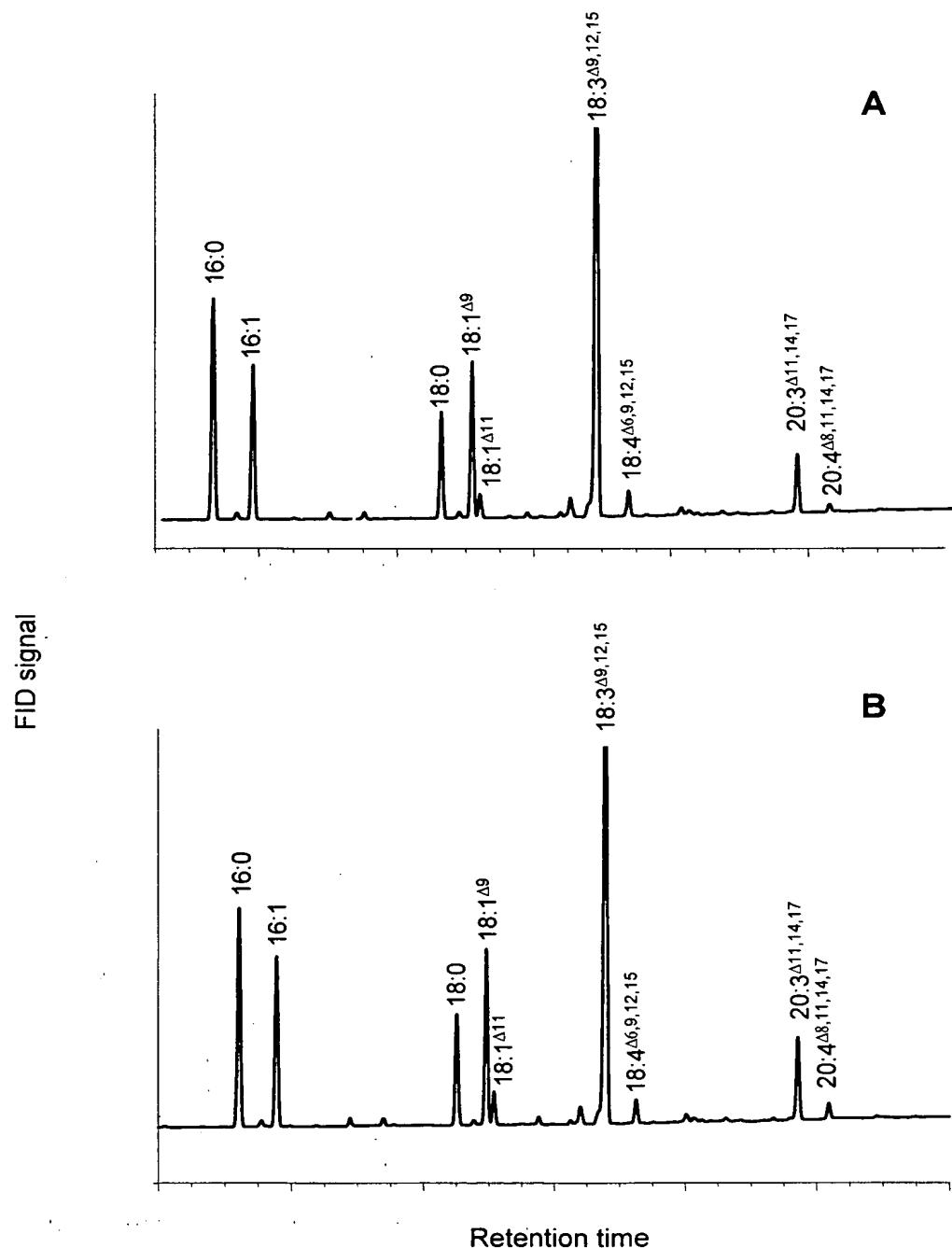
Figure 5: Fatty acid profiles of transgenic C13ABYS86 *S. cerevisiae* cells

Figure 6: Acyl-CoA composition of transgenic INVSc1 yeasts which had been transformed with the vectors pESCLeu PpD6Pse1/pYes2 (A) or pESCLeu-PpD6-Pse1/pYes2-T06E8.1 (B).

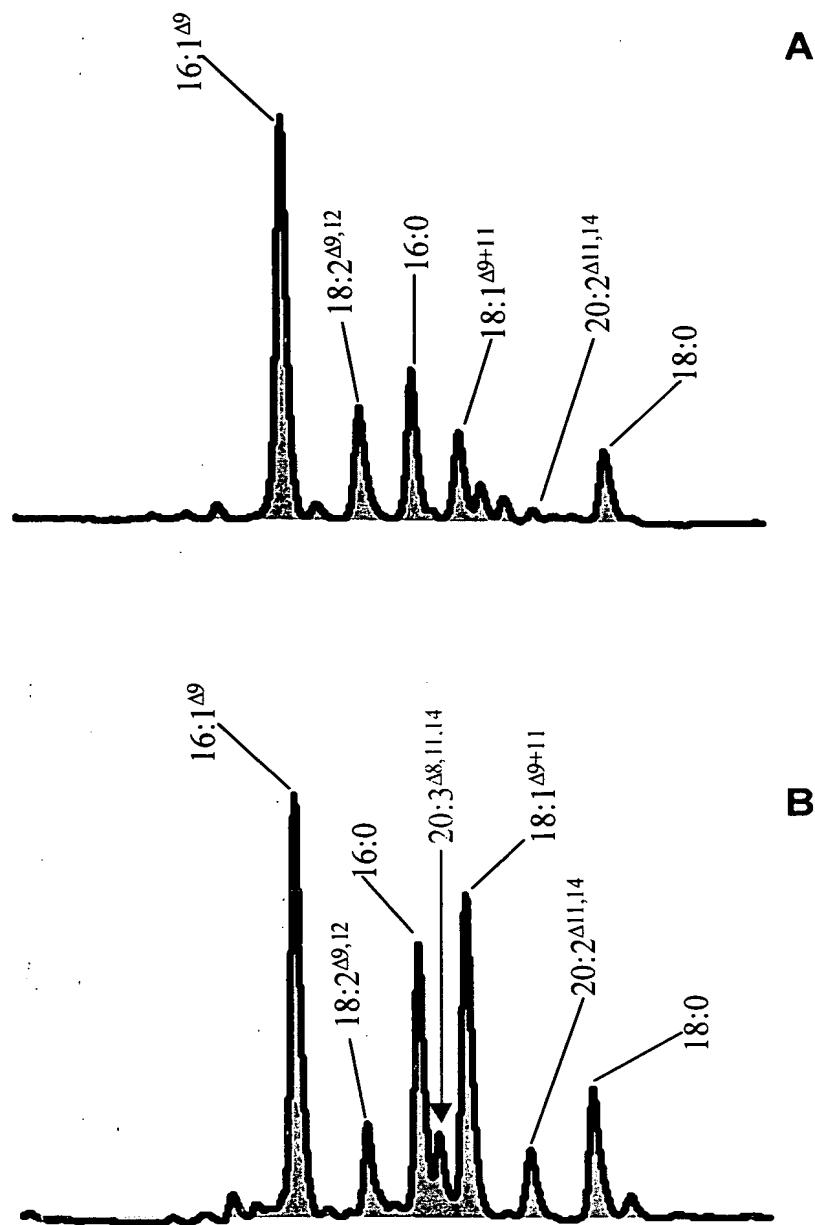


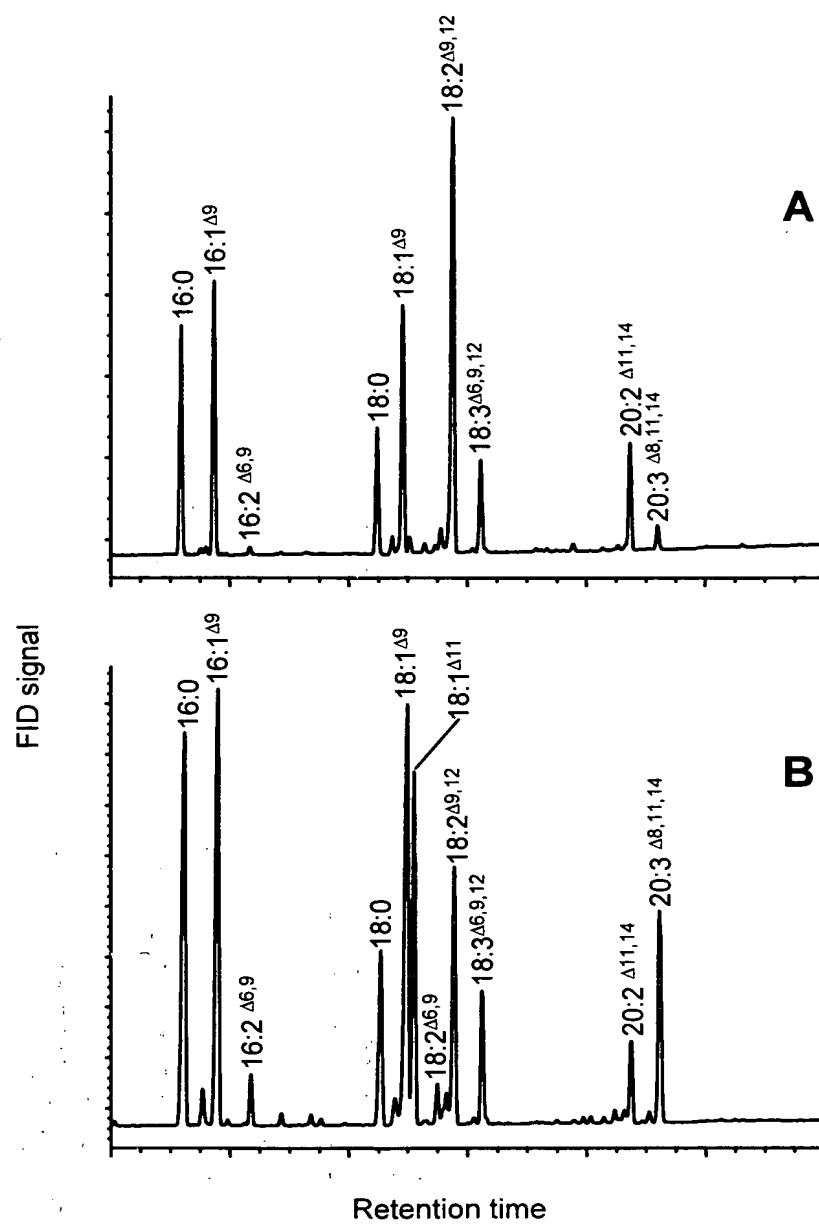
Figure 7: Fatty acid profiles of transgenic INVSc1 *S. cerevisiae* cells

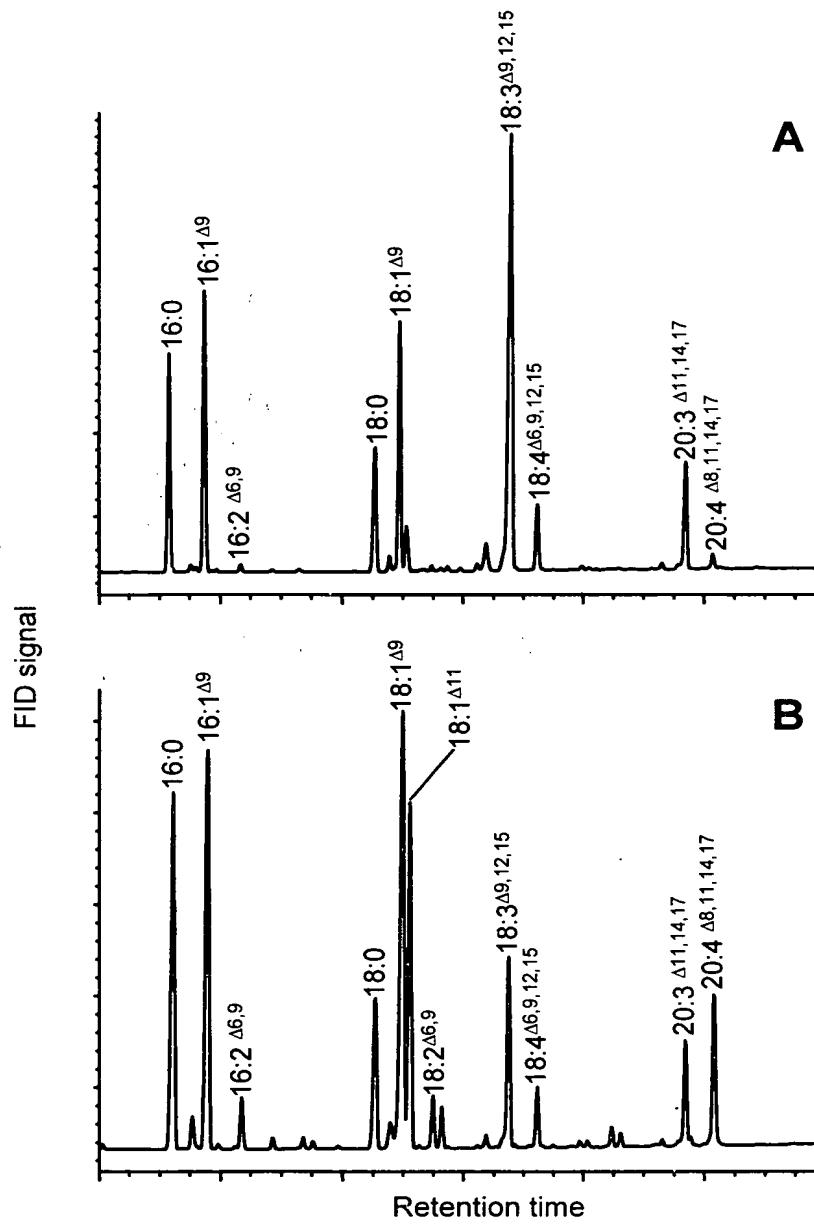
Figure 8: Fatty acid profiles of transgenic INVSc1 *S. cerevisiae* cells.

Figure 9A: Vector map of pGPTV LeB4-700 + T06E8.1

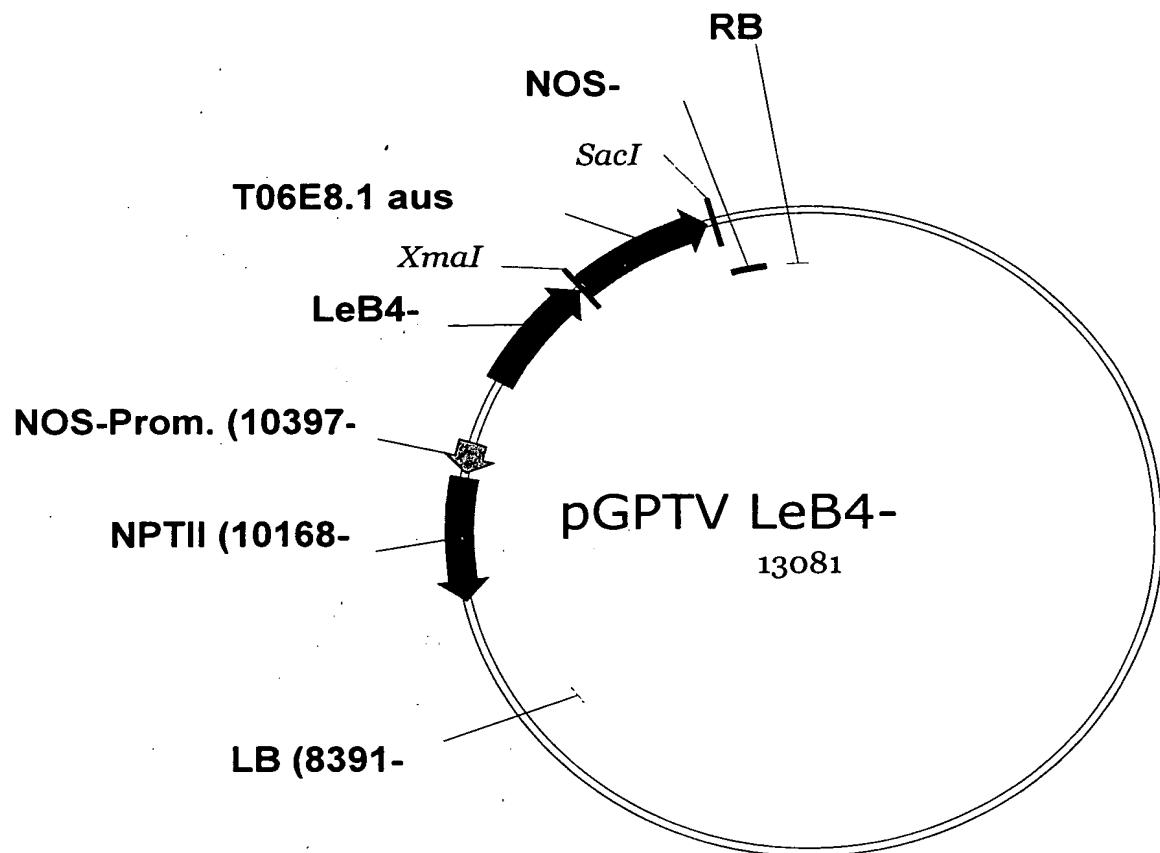


Figure 9B: Vector map of pGPTV USP/OCS-1,2,3 PSE1(Pp)+D6-Des(Pt)+2AT (T06E8-1)

pGPTV/USP/OCS-1,2,3 PSE1(Pp) D6-Des(Pt)-2 AT(T06E8-1)

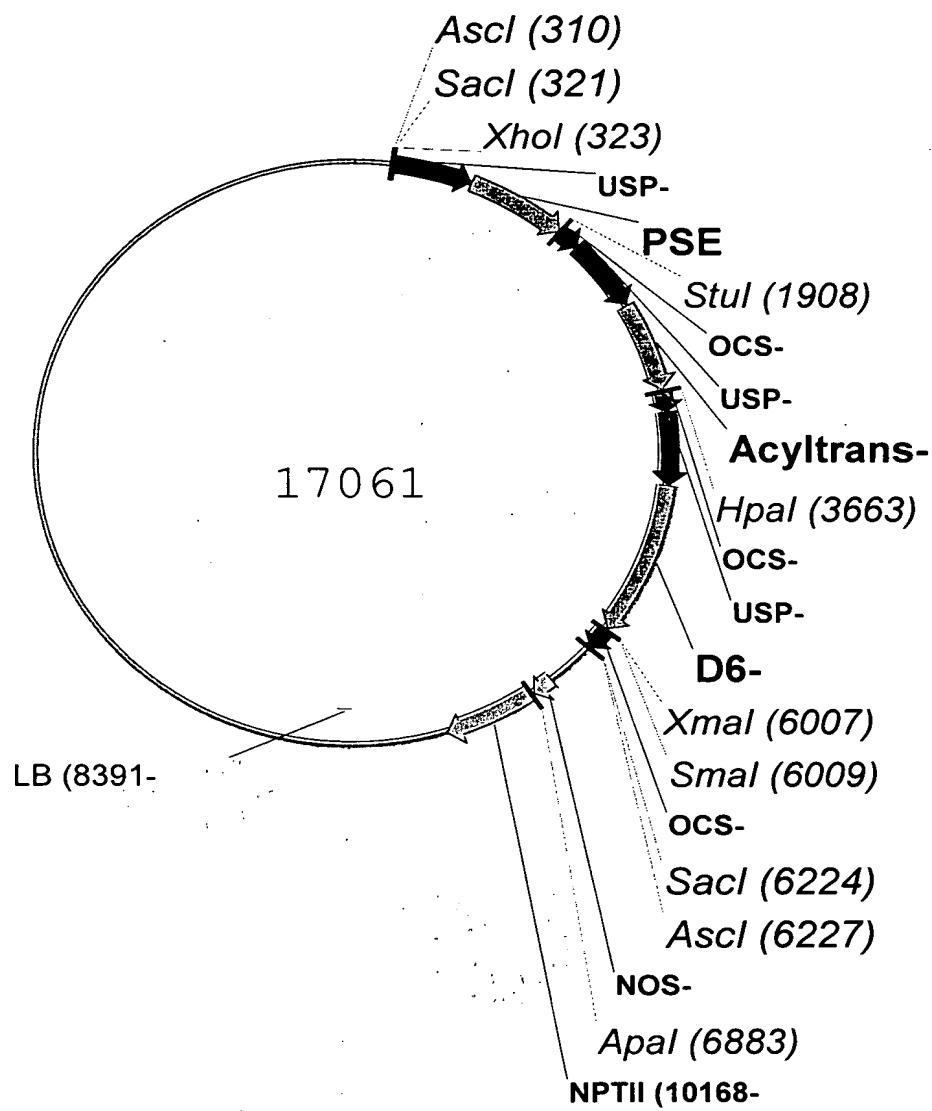


Figure 10A: Biosynthetic pathway of LCPUFAs

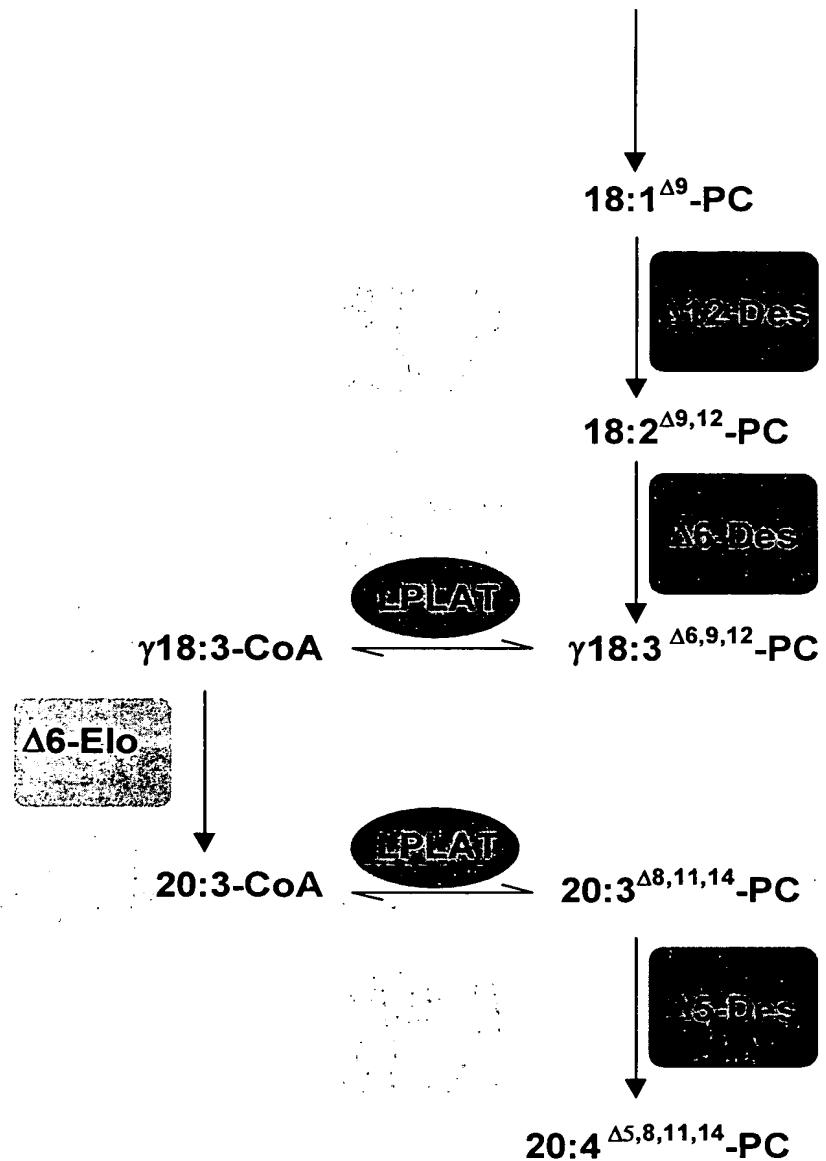


Figure 10B: Biosynthetic pathway of LCPUFAs

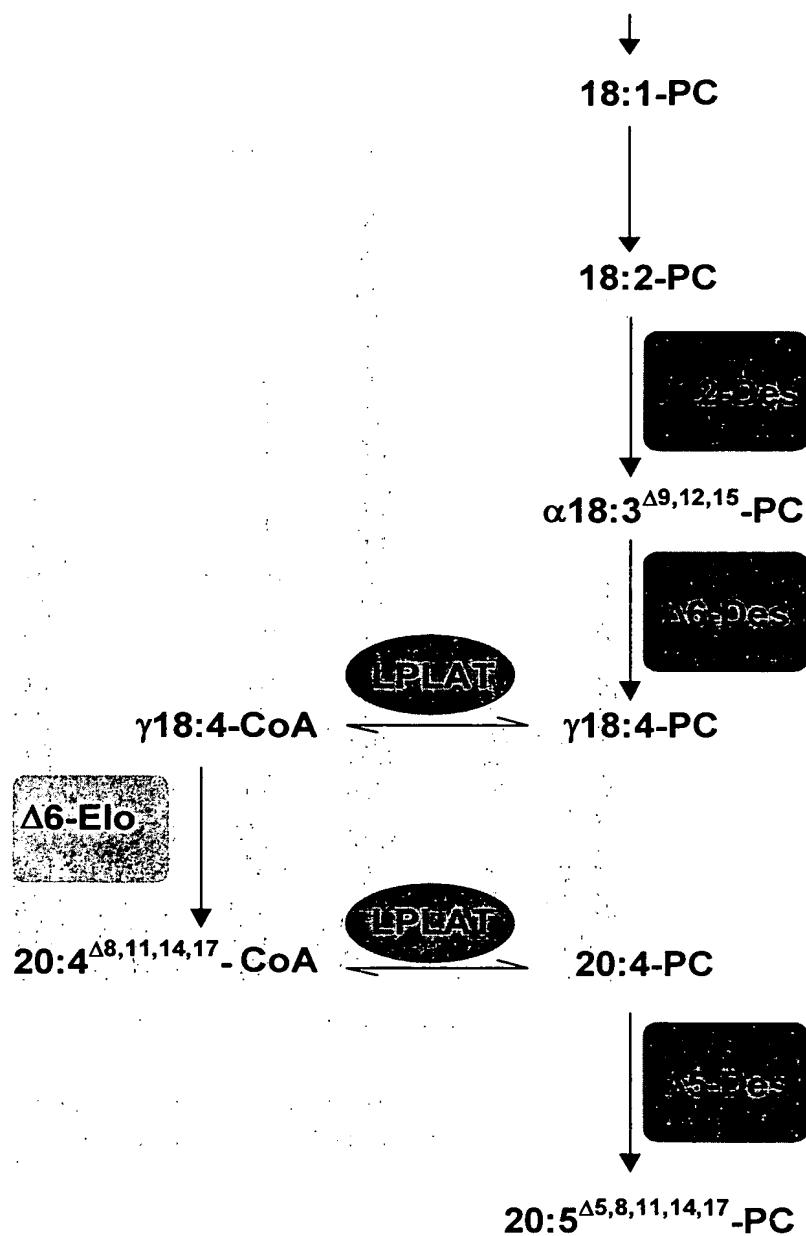


Figure 11: Comparison of GPAT and LPAAT substrate specificities in linseed, sunflower and *Mortierella alpina*

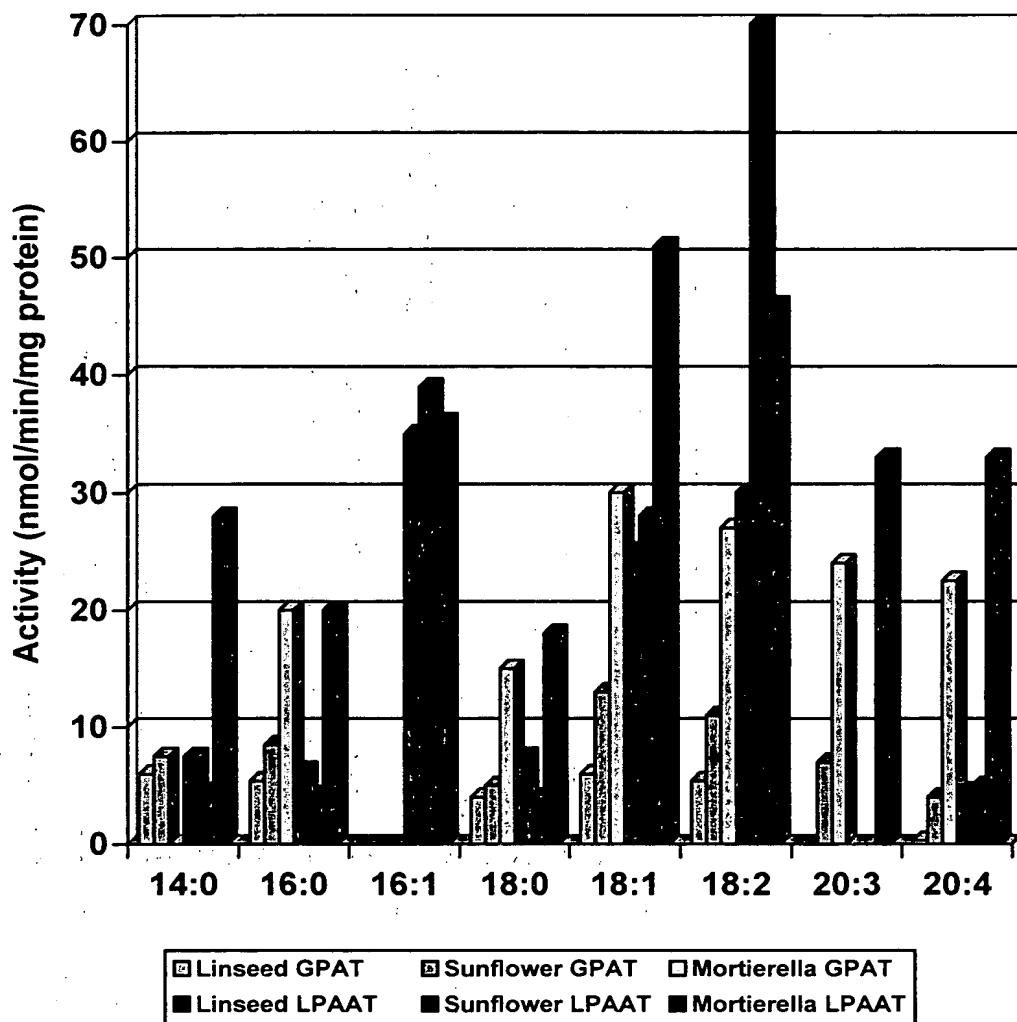
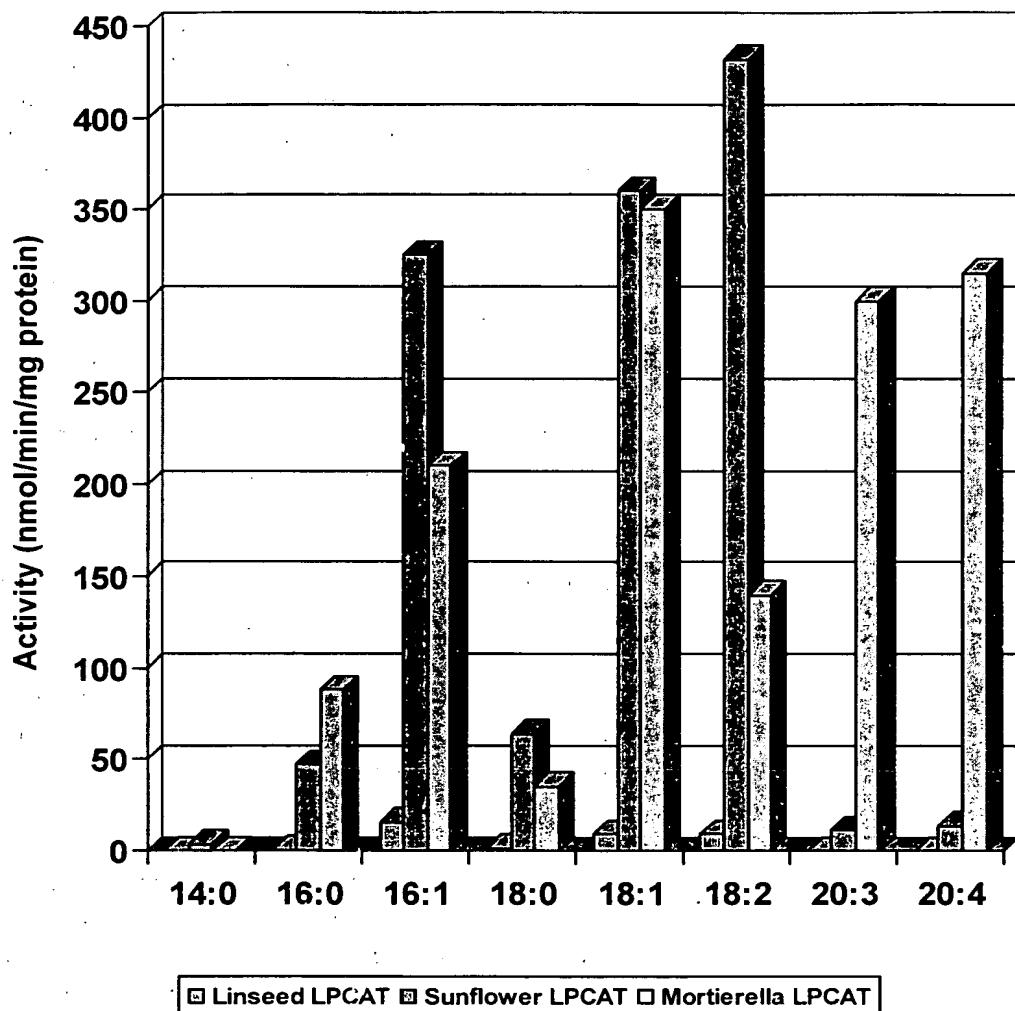


Figure 12: Comparison of LPCAT substrate specificity in linseed, sunflower and - *Mortierella alpina*



15/37

Figure 13: Alignment of SEQ ID NO: 2 with Swiss Prot database

	1	50
Q9JZ47	.....	MSSNKASFFTRL
Q9JU41	.....	MSSNKASFFTRL
Q59601	.....	MSSNKASFFTRL
Q9HW50	.....	MARLRLLLRSARL
SEQ ID NO: 2	.....	MSAWTRAKTAVGL
O35259	METIMDEVTKRTSAEELESWNLLSRTNYNFQYISRLTILWGLGVLI	RY
	51	100
Q9JZ47	RRLCRLAVWLFKTGKNLRGIDGG.CPESRNRAVIELGRGVLAALD....	
Q9JU41	RRLCRLTVWLFKTGKNLRGIDGG.CPESRNRAVIELGRGVLAALD....	
Q59601	RRLCRLTVWLFKTGKNLRGIDGG.CPKSRNRAVIALGKGALAALD....	
Q9HW50	LGLVALGLGLAAVSLRERLPGADVTPLRQLTRWVLARLCAALP....	
SEQ ID NO: 2	LTLAPARIVFLTVLGYGLTVAACTRLGVPKSFVLGLTRCVARLTLWGL	
O35259	CFLLPLRIALAFTGIGLLVVGTTMVGVLPGNRFKEFLSKHVHLMCYRICV	
	101	150
Q9JZ47	..IGLEVGRPAPEHPNG..VLVAANHVSWLDIFAMS.AVYPSSFIAKQEI	
Q9JU41	..IGLEVGRPAPEHPNG..VLVAANHVSWLDIFAMS.AVYPSSFIAKQEI	
Q59601	..IGLEVGRPAPEHPNG..VLVAANHVSWLDIFAMS.AVYPSSFIAKQEI	
Q9HW50	..FEVRVSGEAPRQP....MLWVANHVSWTDIPLLG.ALAPLTFLSKAEV	
SEQ ID NO: 2	GFYHIEVSCDAQGLREWP.RVIVANHVSYLEILYFMSTVHCPSFVMKKTC	
O35259	RALTAIITYHNRKNRPRNNGICVANHTSRIDVIIFASDGYYAMVGQVHGG	
	151	200
Q9JZ47	KSWPVLGKMGQNAGTVFINRNSRR.....DIEPINRAVCETLQRGQ	
Q9JU41	KSWPVLGKMGQNAGTVFINRNSRR.....DIEPINRAVCETLQRGQ	
Q59601	KSWPVLGKMGQNAGTVFINRNSRR.....DIEPINRAVCETLQRGQ	
Q9HW50	RAWPLAGWLAEKAGTLFIRRGSG.....DSRLINQRLAEQLHRGR	
SEQ ID NO: 2	LRVPLVGYIAMELGGVIVDREGGGQSASAIIRDVQEPPRDSSEKHQA	
O35259	LMGVIQRAMVKACPHVWFERSEVK.....DRHLVAKRLTEHVQDKS	
	201	250
Q9JZ47	..NVSFFPEARTSSGLGLPFKAALFQSAIDAGAKVLAVALRYYDETGKR	
Q9JU41	..NVSFFPEARTSSGLGLPFKAALFQSAIDAGAKVLAVALRYYDETGKR	
Q59601	..NVSFFPEARTSSGLGLPFKAALFQSAIDAGAKVLAVALRYYDETGKR	
Q9HW50	..NLLIFPEGTTTNGESLRTFHGRIMASALEAGVAVQPVAISYRRDGVPD	
SEQ ID NO: 2	..PLLVFPEGTTTNGSCLLQFKTGAFR...PG.APVLPVVLEFPIDKARG	
O35259	KLPILIFPEGTCINNTSVMMFKKGSFEIG....ATVYPVAIKY..DPQFG	

	251	300
Q9JZ47	TARPSYADVGLPTCLWRIVSMKKLTIRVDFVCVADAAE.....	
Q9JU41	TARPSYADVGLPTCLWRIVSMKKLTIKVDFVCVADAAE.....	
Q59601	TARPSYADVGLPTCLWRIVSMKKLTIKVDFVCVADAAE.....	
Q9HW50	AQAFFIGDDDLLSHLGRLRGERGSVH1QLLEPIPSQ.....	
SEQ ID NO: 2	DFSPAYESVHTPAHLLRMLAQWRHRLRVRYLPLYEPSAAEKVDADLYARN	
O35259	DAFWNSSKYGMVTYLLRMMTSWAIVCSVWYLPPMTRE.....	

	301	349
Q9JZ47	...SEDRYALKDKIEESIRAVVADDADIAV.....	
Q9JU41	...SEDRYALKDKIEESIRAVVADDADIAV.....	
Q59601	...SEDRYALKDKIEESIRAVVADDADIAV.....	
Q9HW50	...GLDRAELARQAQQAVRLALFGTAAPTQTRRAA.....	
SEQ ID NO: 2	VRDEMARALKVPTVEQSYRDKLVYHADLMPHYQKAGPGALYLYVRPDLL	
O35259	.....KDEDAVQFANRVKSAIARQEDW.....	

17/37

Figure 14: Alignment of SEQ ID NO: 5 with Swiss Prot database

	1	50
Q9C9P8	MEVCGDLKSDNLKNRPLTPLRILRGLMILLVFLSTAFMFLYFAPIAALG	
Q9SFJ1	MEVCGDLKSDNLKNRPLTPLRILRGLMILLVFLSTAFMFLYFAPIAALG	
Q9LHN4	.....MEKKSVNNSDKLSSLIRVLRGIICLMVLVSTAFMMLIFWGFLSAVV	
SEQ ID NO: 5	.....	
Q9SDN3	.....	
Q9XFW4	.....MAMAAAIVPLGILFFISGLVVNLLQAVCYVLV	
	51	100
Q9C9P8	LRLLSVQQSRKVVSILIFGLWLALWPYLTFETVNGTTVVFSGDIIP...VEK	
Q9SFJ1	LRLLSVQQSRKVVSILIFGLWLALWPYLTFETVNGTTVVFSGDIIP...VEK	
Q9LHN4	LRLFSIRYSRKCVSFFFGSWLALWPFLFEKINKTKVIFSGDKVP...CED	
SEQ ID NO: 5	.....MDVVVKVIFAGDKVP...KEN	
Q9SDN3	.....MGKE	
Q9XFW4	RPM SKNTYRKINRVVAETLWLELVWIVDWWAGVKIQVFADDETFRNRMGKE	
	101	150
Q9C9P8	RVLLIANHRTEVDWMLWNIALRKGCGLGYIKYVLKSSLMKLPIFGWGFHV	
Q9SFJ1	RVLLIANHRTEVDWMLWNIALRKGCGLGYIKYVLKSSLMKLPIFGWGFHV	
Q9LHN4	RVLLIANHRTEVDWMLWFWDLALRKQIGNIKYVLKSSLMKLPFGWAFHL	
SEQ ID NO: 5	RVMVMCNHRTEVDWMLIWNLAIRKGKIGYCKYAVKNSVKNLPLFGWAFYV	
Q9SDN3	HALVISNHRSDIDWLGVWVLAQRSGCLGSSLAVMKSSKFLPVIGWSMWF	
Q9XFW4	HALVVCNHRSDIDWLGVWILAQRSGCLGSALAVMKSSKFLPVIGWSMWF	
	151	200
Q9C9P8	LEFIPVERKREVDEPVLLQMLSSFKDPQEPLWLALFPEGTDFTEEKCKRS	
Q9SFJ1	LEFIPVERKREVDEPVLLQMLSSFKDPQEPLWLALFPEGTDFTEEKCKRS	
Q9LHN4	FEFIPVERRWEVDEANLRQIVSSFKDPRDALWLALFPEGTDFTEAKCQRS	
SEQ ID NO: 5	FEFLMLHRKWEVDAPVIKYIDSQDKRDPLWLVVFPEGTDFSEAKRDTG	
Q9SDN3	SEYLFLERSWAKDEGTLKSGVQRLKDFPQPFWLALFVEGTRFTQAKLLAA	
Q9XFW4	SEYLFLERNWAKDESTLQSQLQRLNDFPRFWLALFVEGTRFTEAKLCAA	
	201	250
Q9C9P8	QKFAAEVGLPALSNVLLPKTRGFGVCLEVHLNSLDAVYDLTIAYKPRCP.	
Q9SFJ1	QKFAAEVGLPALSNVLLPKTRGFGVCLEVHLNSLDAVYDLTIAYKPRCP.	
Q9LHN4	KKFAAAEGLPILNNVLLPRTKGFVSCLQELCSLDAVYDVTIGYKTRCP.	
SEQ ID NO: 5	NAIGREKGYPELVNVLQPRTRGFVTCLSQSRCSDLDAVYDLTIAYKTRCP.	
Q9SDN3	QEYAAATGLPVPRNVLI PRTKGFVTAQSQRMSFAPAIYDVTVAIPKSSPA	
Q9XFW4	QEYAAASSELPVPRNVLI PRTKGFVSAVSNMRSFVPAIYDMTVAIPKTSPP	

	251	300
Q9C9P8	SFMDNVFGTDPSEVHIHVRVLLKEIPANEAESSAWLMDSFKLKDQLLSD	
Q9SFJ1	SFMDNVFGTDPSEVHIHVRVLLKEIPANEAESSAWLMDSFKLKDQLLSD	
Q9LHN4	SFLDNVYGIPESEVHIHIRRINLTQIPNQEKDINAWLMNTFQLKDQLLND	
SEQ ID NO: 5	LFINNVFGTDPSEVHIHIRRIPISEIPQSEDGMTQWLYDLFYQKDQMLAS	
Q9SDN3	PTMLRLFEGRPSVHVHIKRHVMRDLPETDEAVAQWCKDIFVAKDALLDK	
Q9XFW4	PTMLRLFKGQPSVHVHIKCHSMKDPPEDEIAQWCRDQFVAKDALLDK	
	301	350
Q9C9P8	FNAQGKFPNQRPEEELSVLKCIATFAGKQQQVTKPSCQKVFLNNQSSDE	
Q9SFJ1	FNAQGKFPNQRPEEELSVLKCIATFAGKQQQVTKPSCQKVFLNNQSSDE	
Q9LHN4	FYSNGHFPNEGTEKEFNTKKYLINCLAVIAFTTICTHLTFFSSMIWFRIY	
SEQ ID NO: 5	FSKTGSFPDSGIE.ESPLNIVEGVCNVALHVVLSGWVFWCLFHSVWLKLY	
Q9SDN3	HTVEQTFGDQQLKVTGRPLKSLLVVTAWACLLILGALKFLYWSSLSSWK	
Q9XFW4	HIAADTFPGQKEQNIGRPIKSLAVVSWACLLTLGAMKFLHWSNLFSSWK	
	351	400
Q9C9P8	KESKKAVAQHPFTDTLDHLFQVEHSISCFLYMHIYNLSTCHLISLYE...	
Q9SFJ1	KESKKAVAQHPFTDTLDHLFQVEHSISCFLYMHIYNLSTCHLISLYE...	
Q9LHN4	VSLACVYLTSAFHNLRSVPLVETAKNSLKLVNK.....	
SEQ ID NO: 5	VAFASLLAFTYFDWRPKPVYSSLRTKRKIV.....	
Q9SDN3	GIAFSALGLGVVTVLMQILIRFSQSERSTPAPVAPTNNKNGESSGKPEK	
Q9XFW4	GIALSAFGLGIITLCMQILIRSSQSERSTPAKVAPAKPKDNHQSGPSSQT	
	401	
Q9C9P8	.....	
Q9SFJ1	.....	
Q9LHN4	.....	
SEQ ID NO: 5	.....	
Q9SDN3	QQ.....	
Q9XFW4	EVEEKQK	

19/37

Figure 15: Alignment of SEQ ID NO: 35 with Swiss Prot database

	1	50
P04180	.....	.....MGP
Q08758	.....	.....MGP
Q9MZ04	.....	.....MGL
Q9DDJ6	.....	.....MGR
Q9Y2B3	.....	.....MGL
SEQ ID NO: 35	MCSISCGSTPQQLCHYRKSGELITRKSRAAIRWWRYGQQCKVLLPLDLIR	
	51	100
P04180	PGSPWQWVTLLLGLLPP.....	.....AAPFWLLNVLFPPHTTPK
Q08758	PGSPWQWVPLLGLLPP.....	.....AAPFWLLNVLFPPHTTPK
Q9MZ04	PGSPWQWVLLLELLLPT.....	.....AAPFWLLNVLFPPHTTPK
Q9DDJ6	TGAGFALLTLLLLLPQP.....	.....ASQFWLFNVLFPPSTPE
Q9Y2B3	HLRPYRVGLLPEGLLFLL.....	.....LLMLLLADPALP.....
SEQ ID NO: 35	SSSQFFIVVLTLLFLFTTCGAVHTAAQDRSFATLSQRSRASLFSVGRAQ	
	101	150
P04180	AELSNHTRPVILVPGCLGNQLEAKLDKPDVVN.WMCYRKTEDFFTIIWLDL	
Q08758	AELSNHTRPVILVPGCLGNQLEAKLDKPDVVN.WMCYRKTEDFFTIIWLDL	
Q9MZ04	AELSNHTRPVILVPGCLGNQLEAKLDKPDVVN.WMCYRKTEDFFTIIWLDL	
Q9DDJ6	APPTNSTPPVVLVPGCLGNQLEAKLDKPDVVN.WMCYRKTEDYFTIWLNL	
Q9Y2B3	...AGRHPVVVLVPGDLGNQLEAKLDKPTVVH.YLCSSKKTESYFTIWLNL	
SEQ ID NO: 35	ARNKHHLAPVVIVPGTGGNQLEARLTADYEANKPWCYSFRKDYFRLWLDV	
	151	200
P04180	NMFLPLGVDCWIDNTRVVVNRSSGLVSNAPGVQIRVPGFGKTYSVYEYLD	
Q08758	NMFLPLGVDCWIDNTRVVVNRSSGLVSNAPGVQIRVPGFGKTYSVYEYLD	
Q9MZ04	NMFLPLGVDCWIDNTRVTVNHSGRVSNAPGVQIRVPGFGKTYPVEYLDN	
Q9DDJ6	NTFLPVGVDCWIDNTRVVVNRTSRKMSNAPGVHIRVPGFGKTYSVYEYLDQ	
Q9Y2B3	ELLLPVIIDCWIDNIRLVYNKTSRATQFPDGVDVRVPFGKTFSLFLDP	
SEQ ID NO: 35	KTLFPPFTTCFADRLSLDYNPQSDAYSNIKGVKTRVPFFGTTEGMEYLD	
	201	250
P04180	SK..LAGYLHTLVQNLVNNNGYVRDETVRAAPYDWRLEPGQQE.....EYY	
Q08758	SK..LAGYLHTLVQNLVNNNGYVRDETVRAAPYDWRLEPGQQE.....EYY	
Q9MZ04	SK..LAGYMHTLVQNLVNNNGYVRDETVRAAPYDWRLGPKQQE.....EYY	
Q9DDJ6	SK..LAGYLHTLVQNLVNNNGYVRDQTVRAAPYDWRVGPQEQP.....EYF	
Q9Y2B3	SKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENG.....PYF	
SEQ ID NO: 35	SLKFLTGYMIHLVNALKAHGYENGKSLYGAPYDFRFAPGPHASNVALEYL	

20/37

	251	300
P04180	RKLAGLVEEMHAAYG . KPVFLIGHSLGCLHLLYFLLRQPQAWKDRFIDGF	
Q08758	HKLAGLVEEMHAAYG . KPVFLIGHSLGCLHLLYFLLRQPQAWKDRFIDGF	
Q9MZ04	RDLARLVEEMHATYG . KPVFLIGHSLGCLHLLHQPQSWKDRFIDGF	
Q9DDJ6	QNLKALIEEMHDEYQ . QRVFLIAHSMGNLNLYFLLQQRQAWKDQYIGGF	
Q9Y2B3	LALREMIEEMYQLYG . GPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAF	
SEQ ID NO: 35	SEQ ID NO: 35 KDLKDLIETAYSVNANEPPVILAHSMGLWTLFFLNQQSMEWRNKYVSRF	
	301	350
P04180	ISLGAPWGGSIKPMVLASGDNQGIPIMSSIKLKEEQRITTS PWMF PSSR	
Q08758	ISLGAPWGGSIKPMVLASGDNQGIPIMSSIKLKEEQRITTS PWMF PSSR	
Q9MZ04	ISLGAPWGGSIKPMQVLASGDNQGIPIMSSIKLKEEQRITTS PWMF PSS	
Q9DDJ6	ISLGAPWGGSVKPLRVLASGDNQGIPLMSNIKLREEQRMTTS PWMF PTS	
Q9Y2B3	VSLGAPWGGVAKTLRVLASGDNNRIPVIGPLKIREQQRSAVSTS WLLPYN	
SEQ ID NO: 35	SEQ ID NO: 35 VSVATPWGGAVEQMMTFASGNPEGVPFVNLSLVREEQRRSESNLWLLPVR	
	351	400
P04180	MAWPEDHVFISTFSNYTGRDFQRFFADLHFEEGWYMWLQ . SRDLLAGLP	
Q08758	LAWPEDHVFISTPSFNYTGRDFQRFFADLHFEEGWYMWLQ . SRDLLAGLP	
Q9MZ04	EVWPEDHVFISTPSFNYTIRDYQRFFDVHFEEGWYMWLQ . SRDLLAGLP	
Q9DDJ6	LAWPEDHIFI STPSYNTYRDYKQFFTDVNLEDGWYMWED . MKDLLKGLP	
Q9Y2B3	YTWSPEKVFVQTPTINYTLRDYRKFFQDIGFEDGWLMRQD . TEGLVEATM	
SEQ ID NO: 35	SEQ ID NO: 35 RCFR . DRPLVITSSRNYTAGDMEQFLCDIGFPEGVAPYKSRIPLTDILQ	
	401	450
P04180	APGVEVYCLYGVGLPTPRTYIYDHGFPTDPVGVLYEDGDDTVATRST . E	
Q08758	APGVEVYCLYGVGLPTPRTYIYDHGFPTDPDVLYEDGDDTVATRST . E	
Q9MZ04	APGVEVYCLYGVGLPTPSTYIYDHDFPYTDPLDVLYEDGDDTVATRSM . E	
Q9DDJ6	PPGVDTYCLYGTGYPTVETYIYDEHFPYEDPVDMIYGDGDDTVNRRSS . E	
Q9Y2B3	PPGVQLHCLYGTGVPTPDSFYYES . FPD RDPK . ICFG DGDGTVN LKSA . L	
SEQ ID NO: 35	SEQ ID NO: 35 PPQVPVTI HGYGVPTAETLSYK . KGF DNHPEITEGDGDGTVN VCSLTA	
	451	500
P04180	LCGLWQGRQPQPVHLLPLHGIQHLMVFSNLTLEHINAILLGAYRQGPPA	
Q08758	LCGLWQGRQPQPVHLLPLRGIQHLMVFSNQTLLEHINAILLGAYRQGPPA	
Q9MZ04	LCSQWQGRQPQPVHLLPLHRIQHLMVFSNQTLLEHINDILLGAYRHGNPV	
Q9DDJ6	LCKRWRNQQKQKVHIIQELRGIDHLMVFSNLTSSINEILLGSSQVGAGT	
Q9Y2B3	QCQAWQSRQEHQVLLQELPGSEHIELANATTLAYLKRVLLGP . . . . .	
SEQ ID NO: 35	SEQ ID NO: 35 VVEEWERVAGQELEMIALHGKQHMQILHDDHSVQVIVDAILNVTPQEQLM	
	501	524
P04180	SPTASPEPPPPE . . . . .	
Q08758	SLTASPEPPPPE . . . . .	
Q9MZ04	PPAASPRPLTPE . . . . .	
Q9DDJ6	KEHGE LGQMGALKSSLEAGRRGKN	
Q9Y2B3	FH . . . . .	
SEQ ID NO: 35	SEQ ID NO: 35 FH . . . . .	

## 21/37

Figure 16: Alignment of SEQ ID NO: 23 with Swiss Prot database

1	50
P10349	.....
Q9FEP9	.....MFILSSSSSTLPSAPPFSSSTSIFLSFSRVSLPPSSSSLK...
Q39639	MFILSAVSSSSSSSVPSSLPPFSLSPSISLSFSRVSLPPSSSSSSL
Q9FEQ0	.....MFILSSSSLPPLSPLSLSRVSLPPSSSSLN..
Q9M4V1	.....MLVPSALPRVSRVSARFSVSGVGSSPALSSRS
SEQ ID NO: 23	.....MPSLFRAKRNGRRTPGNAVTN...
51	100
P10349	.....MAELIQDKESAQSAATAAAAS
Q9FEP9	..LLPLSLQFGPPKLAS .SCSLRFSASRAMAELIQDKESAQSAATAAAAS
Q39639	KLFLPLSLHFTPPKLSSPHSFLRFSAASRAMAELIQDKESAHTPSTTDVTR
Q9FEQ0	..LLPLSPHFQPPNLAC ...SCSVASRSTAELLHDFKHSAAHTAASADEAR
Q9M4V1	CTSLDSSVRSSLRRCPCGIYTSRTKAVVEAVESKASAREWRSAVKRAVLA
SEQ ID NO: 23	.....FGKSEFH.....R..EIS...GSTRATTQVAEATTAGLRE
101	150
P10349	SGYERRNEPAHSRKFLDVRSEEELLSCIKKETEAGKLPPNVAAGMEELYQ
Q9FEP9	SGYERRNEPAHSRKFLDVRSEEELLSCIKKETEAGKLPPNVAAGMEELYQ
Q39639	N.....DPPHSRAFLDLRSEEELLSCIRRETEAGKLPSNVAAGMEELYQ
Q9FEQ0	N.....HLPHSRAFLDVRSEQELLSYIRREAEAGKLPSNVAAGMEELYQ
Q9M4V1	SDTGAEVEVGHSRSFLRARSEEELLSYIRKEVETGRLSSDIANGLEELYY
SEQ ID NO: 23	TIEDRAIIDGHSHSFEGIQSEEELMQVIEKEVESGRPLKRAGAGMVELYR
151	200
P10349	NYRNAVIESGNPKADEIVLSNMTVALDRILLDVEDPFVFSSHHKAIREPF
Q9FEP9	NYRNAVIESGNPKADEIVLSNMTVALDRILLDVEDPFVFSSHHKAIREPF
Q39639	NYKNAVFESGNPKADEIVLSNMTVALDRILLDVEDPFMFSPHHKAIREPF
Q9FEQ0	NYKNAVLKGSGNPKADEIVLSNMTVALDRILLDVEEPFVSPHHKAVREPF
Q9M4V1	NYRNAVLOSGDPRANKIILSNMAVAFDRILLDVEDPFTSPHHQAIREFP
SEQ ID NO: 23	NYRDAVVSSGVENAMDIVVKVMSTVLDRILLQFEEPFTFGSHHKRMVEPY
201	250
P10349	DYYIFGQNYIRPLIDFGNSFVGNLSLFKDIEEKLQQGHNVVLISNHQTEA
Q9FEP9	DYYIFGQNYIRPLIDFGNSFVGNLSLFKDIEEKLQQGHNVVLISNHQTEA
Q39639	DYYTFGQNYVRPLIDFENSFVGNLSLFKDIEEKLHQGHNVVLISNHQTEA
Q9FEQ0	DYYTFGQNYVRPLIDFGNSFVGNPFLFKDIEEKLHQGHNVVLISNHQTEA
Q9M4V1	DYYMFGQNYIRPLIDFRRSYIGNISIFSDMEEKLQQGHNIVLMSNHQTEA
SEQ ID NO: 23	DYYTFGQNYVRPLLDFRNSYLGNLKIFDQIEKNLKEGHNVIFLSNHQTEA

22/37

	251	300
P10349	DPAIISLLLEKTNPYIAENTIFVAGDRVLA DPLCKPFSIGRNLICVYSKK	
Q9FEP9	DPAIISLLLEKTNPYIAENTIFVAGDRVLA DPLCKPFSIGRNLICVYSKK	
Q39639	DPAIISLLLEKTNPYIAENMIYVAGDRVIA DPLCKPFSIGRNLICVYSKK	
Q9FEQ0	DPAIISLLLEKTPYIAENMIYVAGDRVIVDPL CKPFSIGRNLICVYSKK	
Q9M4V1	DPAIIALLERTNSHIAETMVFVAGDRVLT DPLCKPFSIGRNLICVYSKK	
SEQ ID NO: 23	DPAVMALLLEHSHPYLAENLTYVAGDRV VLDPFCKPFSIGRNLICVYSKK	
	301	350
P10349	HMFDIPELTETKRKANTRSLKEMALLLRGG SQLIWIAPSGGRDRPDPSTG	
Q9FEP9	HMFDIPELTETKRKANTRSLKEMALLLRGG SQLIWIAPSGGRDRPDPSTG	
Q39639	HMLDIPELAETKRKANTRSLKEMALLLRGG SQLIWIAPSGGRDRPDPSTG	
Q9FEQ0	HMFDIPELAETKRKANTRSLKEMALLLRGG SQLIWIAPSGGRDRLDPSSG	
Q9M4V1	HMDDVPELIEMKRRANTRSLKEMALLLRGG SQLIWIAPSGGRDRPDPSTG	
SEQ ID NO: 23	HIHDVPDLAEMKIKANAKTLRQMTILLRQGG QYYG.....	
	351	400
P10349	EWYPAPFDASSVDNMRRLLIQHSDVPGH LFPLALLCHDIMPPPSQVEIEIG	
Q9FEP9	EWYPAPFDASSVDNMRRLLIQHSDVPGH LFPLALLCHDIMPPPSQVEIEIG	
Q39639	EWYPAPFDASSVDNMRRLLQHSGAPG HLYPLALLCYDIMPPPSQVEIEIG	
Q9FEQ0	EWLPAPFDASSMDNMRRLLIQHSGV PGHLCPLALLCYDIMPPPSKVEIEIG	
Q9M4V1	EWHPAPFDVSSVDNMRRLVEHSSV PGHIYPLSLLCYEVMPQQVEKQIG	
SEQ ID NO: 23	.....	
	401	450
P10349	EKRVIAFNGAGLSVAPEISFEEIAATH KNPEEVREAYSKALFDVAMQYN	
Q9FEP9	EKRVIAFNGAGLSVAPEISFEEIAATH KNPEEVREAYSKALFDVAMQYN	
Q39639	EKRVISFNGTGLSVGPEISFDEIAASR DNPDEVREAYSKALYDSVAKQYN	
Q9FEQ0	EKRVISFNGVGLSLAPAISFEAIAATH RNPDEAREAYSKALFDVSMQYN	
Q9M4V1	ERRTISFHGVGLSVAPELFN ELTAGCETPEEAKEAFSQALYN SVGEQYN	
SEQ ID NO: 23	.....	
	451	476
P10349	VLKTAISGKQGLGASTADVSLSQPW.	
Q9FEP9	VLKTAISGKQGLGASTADVSLSQPW.	
Q39639	VLKAAIDGKQELEASVADVSLSQPW	
Q9FEQ0	VLKAAIYGRQALR ASTADVSLSQPW	
Q9M4V1	VLKSAIHEH RGLNASNSII SLSQPWQ	
SEQ ID NO: 23	.....	

23/37

Figure 17: Alignment of SEQ ID NO: 27 with Swiss Prot database

SEQ ID NO: 27	1	50
Q9XFW4	MEGGGSIIALPLGLMFLSGFFINILQLLSVLFILPFSRRAYRVVNIMM	
Q40119	.MAMAAAIVPLGILFFISGLVVNLLQAVCYVLVRPMSKNTYRKINRVVA	
Q9SDN3	MAIPAAAFIVPISLLFFMSGLVVNFIQAVFYVLVRPISKDTYRRINTLVA	
Q41745	.....	
Q9SYC8	MAIPLVLVVLPLGLLFLSGLIVNAIQAVLFVTIRPFSKSFYRRINRFLA	
SEQ ID NO: 27	51	100
Q9XFW4	EVLWSELIWLLDWWANVKVKVYTPKESWEHLGKEHALLICNHRSDIDWLV	
Q40119	ETLWLELVWIVDWWAGVKIQVFADDETFNRMGKEHALVVCNHRSDIDWLV	
Q9SDN3	ELLWLELVVVIDWWAGVKVQLYTDTESFRLMGKEHALLICNHRSDIDWLI	
Q41745	.....MGKEHALVISNHRSDIDWLV	
Q9SYC8	ELLWLQLVWWWDWWAGVKVQLHADEETYRSMGKEHALIISNHRSDIDWLI	
SEQ ID NO: 27	101	150
Q9XFW4	GWIIAQRLGCLGGTRAVMKKSTKFLPVIGWSMWFSSEYVFLSRDWAKDEKV	
Q40119	GWILAQRSGCLGSALAVMKKSSKFLPVIGWSMWFSSEYLFERNWAKDEST	
Q9SDN3	GWVLAQRCGCLSSSIAMKKSSKFLPVIGWSMWFSSEYLFERNWAKDENT	
Q41745	GWVLAQRSGCLGSSLAVMKKSSKFLPVIGWSMWFSSEYLFERSWAKDEGT	
Q9SYC8	GWVMAQRVGCLGSSLAIMKKEAKYLPPIIGWSMWFSDYIFERSWAKDEKT	
SEQ ID NO: 27	151	200
Q9XFW4	LKNQYSSLKGFPRTLWVALFVEGTRFTKAKLEAAQKFAADTGLRVPRHVL	
Q40119	LQSGLQRLNDFPRPFWLALFVEGTRFTEAKLKAAQEYAAASSELPVPRNVL	
Q9SDN3	LKSGLQRLNDFPKPFWLALFVEGTRFTQAKLLAAQEYAAASAGLPVPRNVL	
Q41745	LKSGVQRLKDFPRPFWLALFVEGTRFTPAKLLAAQEYAAASQGLPAPRNVL	
Q9SYC8	LKAGFKRLEDFPMTFWLALFVEGTRFTQEKLEAAQEYASIRSLPSPRNVL	
SEQ ID NO: 27	201	250
Q9XFW4	IPRTKGFVSAVENLREFPVVYDMTVAISKELPNPTMIRIFRGQPSVHV	
Q40119	IPRTKGFVSAVNMRSPVPAIYDMTVAIPKTSPPPTMLRLFKQPSVHV	
Q9SDN3	IPRTKGFVSAVNMRSPVPAIYDLTVAIPKTTEQPTMLRLFRGKSSVHV	
Q41745	IPRTKGFVTAVSQMRSPVPAIYDVTVAIPKSSPAPTMRLFEGRPSVHV	
Q9SYC8	IPRTKGFVSAVSIMRDFVPAIYDTTVIVPKDSPQPTMLRILKGQSSVIHV	

24/37

	251	300
SEQ ID NO: 27	HVRVPMSDLPEGANAISKWCHDAFHIKDDRLEQHEKENTFGEDLYIPIE Q9XFW4 HIKCHSMKDLPEPEDEIAQWCRDQFVAKDALLDKHIAADTFPGQKEQNIG Q40119 HLKRHLMKDLPKTDDGVAQWCKDQFISKDALLDKHVAEDTFSGLEVQDIG Q9SDN3 HIKRHVMRDLPETDEAVAQWCKDIFVAKDALLDKHHTVEQTFGDQQLKVTG Q41745 RMKRHAMSEMPKSDEDVSKWCKDIFVAKDALLDKHLATGTFD.EEIRPIG Q9SYC8 QMRRHKMSELPETDGGIAQWCQDLFITKDAQLEKYFTKDVFSDLEVHQIN	
	301	350
SEQ ID NO: 27	RPLKPLIIVVISWAITLLAAAWWFLRR..VLSTWKGIAWVAGVLVVVMLCV Q9XFW4 RPIKSLAVVVSWACLLTLGAMKFLHWSNLFSSWKGIALSAFGLGIITLCM Q40119 RPKSLVVVVSWMCLLCGLVKFLQWSALLSSWKGMITTFVLGIVTVLM Q9SDN3 RPLKSLLVVTAWACLLILGALKFLYWSSLSSWKGIAFSALGLGVVTVLM Q41745 RPVKSLLVTLFWSCLLLFGAIEFFKWTQLLSTWRGVAFTAAGMALVTGVM Q9SYC8 RPIKPLIVVIWLGFLVFGGFKLLQWLSIVASWKIILLFVFFLVIATITM	
	351	391
SEQ ID NO: 27	QILVMSSQSERSSDPAAKKANQKQAASVAHLGKD..... Q9XFW4 QILIRSSQSERSTPAKVAPAKPKDNHQSGGPSSQTEVEEKQK Q40119 HILIRSSQSEHSTPAKTRARQTAENPK..... Q9SDN3 QILIRFSQSERSTPAPVAPTNKNKGESSGKPEKQQ..... Q41745 HVFIMFSQAERSSSARAARNRVKKE..... Q9SYC8 QILIQSSESQRSTPAKRPLQEQLISA.....	

25/37

Figure 18: Alignment of SEQ ID NO: 8 with Swiss Prot database

	1	50
SEQ ID NO: 8	MESTADVGMSDDDPILLNGLETPLLAEPPLGERPTIGPEAPVNPFHEPDG	
P42322	.....	
Q9NWK7	.....	
Q9XFJ4	.....MGQRREDIRTLSNEYEVTDIPRRGGLSVVRRGTRRRTLHSGQHHE	
O35259	.....	
Q9FF57	.....	
	51	100
SEQ ID NO: 8	GWKTNNEWNYFQMMKSILLIPLLVLVLSMITIVAFGYWIRICLIGVTD	
P42322	.....	
Q9NWK7	.....	
Q9XFJ4	VVAIKTLR.RFGPPPAPPEKKSLNKSRVPQAALISETLLTNELLVMIKIVE	
O35259	.....METIMDDEVTKRTSAEELESWNLLSRTNYN.	
Q9FF57	.....MIEQLGLIIIMGLIHYQSERVKPREWLKLSSSENSR	
	101	150
SEQ ID NO: 8	PLFKPFNPCCRFLWGLRILVARAVMFTMGYYYIPIKGKPAHRSEAPIIVS	
P42322	.....	
Q9NWK7	.....	
Q9XFJ4	DVS PHPNVIHLYDVCEPSSGVHLILECSGGELFDRIAGQARYNEEGAAA	
O35259	...FQYISLRLTILWGLGVLIRYCFLLPLRIALAFTGIGLLVVGTTMVGY	
Q9FF57	LG.NTKTNHRRSFTGDVSYEQRDLLDISPTLTEAAGAIVDFHCFKTCRCF	
	151	200
SEQ ID NO: 8	NHIGFLDPIFVFYRHLPAIVSAKENVEMPIIGLFLQALQIIPVDRTDAQS	
P42322	.....	
Q9NWK7	.....	
Q9XFJ4	VVRQIAKGLLEALHGASIVHRDLKPENCLFLNKDENSPLKIMDFGLSSIED	
O35259	LPNGRFKEFLSKHVHLMCYR.....	
Q9FF57	TLAFGWIIFLSLFIPVNALLK.....	
	201	250
SEQ ID NO: 8	RHHAAGNVRRRAVDNMWSHVMLFPQGTTTNGRAIIAFKTGAFSPGLPVQP	
P42322	.....	
Q9NWK7	.....	
Q9XFJ4	FANPVVGLFGSIDYVSPEALSREKITTKSDIWSLGVILYILLSGYPPFIA	
O35259	.....	
Q9FF57	.....GQDRLRKIER	

26/37

	251	300
SEQ ID NO: 8	MVIRYPHKYVNPSWCDQGGPLVVVLQLMTQFINHMEVEYLPMVKPTVREM	
P42322	.....	
Q9NWK7	.....	
Q9XFJ4	PSNRQKQQMILNGQFSFDEKTWKNISSSAKQLISSLLKVDPNMRPTAQEI	
O35259	ICVR.ALTAIITYHN.....	
Q9FF57	VLVEMICSFFVASWTG.....	
	301	350
SEQ ID NO: 8	KYPHEFASRVRSEMAKALGIVCTEHSDL...IKLALAAEKLKQPSGRSL	
P42322	.....MGTNTSSLRP	
Q9NWK7	.....MGN	
Q9XFJ4	LEHPWVTGDLAKQEQM岱EIVSRLQSFNARRKFRAAAMASILSSSFLRT	
O35259	.....RKNRPRN.....GG	
Q9FF57	.....VVKYHGPRPSIRP...KQ	
	351	400
SEQ ID NO: 8	VEFARMEKLFRLLDFPTAKEYLEKFSAMDRTHSGF..VTFEEELCTALDLP.	
P42322	EEVEEMQKGTNFTQKEIKKLYKRFKKLDKGNGT..ISKDEFMLIPELA.	
Q9NWK7	ENSLPMELCSNFDPDEIKRLGKRFRKLDLDNSGS..LSVDEFMLPELQ.	
Q9XFJ4	KKLKLLVGSYDLKPEELENLSHNFKKICKNGENSTLLEEEVLKAMEMSS	
O35259	ICVANHTSRIDVIIFASDGYYAMVGQVHGLMVIQRAMVKACPHVWFE.	
Q9FF57	VYVANHTSMIDFIVLEQMTAFAVIMQKHPGVGLLQSTILEVGCIWFN.	
	401	450
SEQ ID NO: 8	RSPITKQVFNLFDKDGHGSINREFLAGLAFVSSHTSFSSTMEEAFKACD	
P42322	VNPLVKRVISIFDENGDGSVNFKEFIAALSVFNAQGDKQRKLEFAFKVYD	
Q9NWK7	QNPLVQRVIDIFDTDGNGEVDFKEFIEGVSQFSVKGDKLSKLRFAFKIYD	
Q9XFJ4	LVPLAPRIFDLFDNNRDGTVDMREIIGGFSSLKYSQGD.DALRLCFQVYD	
O35259	RSEVKDRHLVAKRLTEHVQDKSKLPILIFPEGTCINNT.SVMMFKKGSFE	
Q9FF57	RSEAKDREIVAKKLRDHVQGADSNPLLIFPEGTCVNNN.YTVMFKKGAFE	
	451	500
SEQ ID NO: 8	VNGDGTLSRDEVERSLLDIFPELPI.....TVFKLFDTLDINHDEKIS	
P42322	IDGDGYISNGELFTVLKMMVGNNLSD.VQLQQIVDKTILEADEDGDGKIS	
Q9NWK7	MDKDGYISNGELFQVLKMMVGNNLKD.TQLQQIVDKTIIHADADGDGKIS	
Q9XFJ4	TDRSGCISKEEVESMLRALPEDCLPINITEPGKLDEIFDLMDANSDGKVT	
O35259	IGATVYPVAIKYDPQFGDAFWNSSKYG.....MVTYLLRMMTSWAIVCSV	
Q9FF57	LDCTVCPIAIKYNKIFVDAFWNSRKQS.....FTMHLLQLMTSWAVVCEV	

27/37

	501	550
SEQ ID NO: 8	WEEFSSFLQRNPEYLAIIIYAHPTLLKPPTSTS.....	
P42322	FEEFAKTLSHQDLENKMTIRL.....	
Q9NWK7	FEEFCAVVGNMDVHKMVVDV.....	
Q9XFJ4	FDEFKAAMQRDSSLQDVVLSSLRPN.....	
O35259	WYLPPTREKDEDAVQFANRVKSAIARQEDW.....	
Q9FF57	WYLEPQTIRPGETGIEFAERVRDMISLRAGLKKVPWDGYLKYSRPSPKHS	

	551	568
SEQ ID NO: 8	.....	
P42322	.....	
Q9NWK7	.....	
Q9XFJ4	.....	
O35259	.....	
Q9FF57	ERKQQSFAESILARLEEK	

28/37

Figure 19: Alignment of SEQ ID NO: 10 with Swiss Prot database

Q24214	.....	50
P28470	.....	
SEQ ID NO: 10	MTSTENTAMFTEDTSTLNGSTEANHAEFPLGERPTIGPEPPVNPFHESST	
O35259	.....METIMDDEVTKRTSAEEL	
Q9XFJ4	MGQREDIRTLSNEYEVTDIPRRGGLSVVRRGTRRRTLHSGQHHEVVAIKT	
Q24214	.....	100
P28470	.....	
SEQ ID NO: 10	WSIPQVIKTILLVPLLVIRLLSMFALMMLGYICVKVAMIGCKDPLFKPFN	
O35259	ESWNLLSRTNYNFQYISLRLTILWGLGVLIIRYCFLLP.....	
Q9XFJ4	LRRFGPPPAAPEKKSLNKS RVPQAA LISETLLTNELLVMIKIVEDVSPHPN	
Q24214	.....	150
P28470	.....	
SEQ ID NO: 10	PLRRLLLVSVRLIARGVMVAMGYYYILVKGKPAHRSVAPIIVSNHIGFVD	
O35259	.....LRIALAF TGIGLLVVG.....TTMVG...	
Q9XFJ4	VIHLYDV CEDPSGVHLILELCSGGELFDRIAGQARYNEEGAAAVVRQIAK	
Q24214	.....	200
P28470	.....	
SEQ ID NO: 10	PIFVFYRHL PVIVSAKEIVEMPIIGMFLQALQIIPVDRINPASRHAAGN	
O35259	.....YLPNGRFKEFLSKH...	
Q9XFJ4	GLEALHGASIVHDLKPENCLFLNKDENSPLKIMDFGLSSIEDFANPVVG	
Q24214	.....	250
P28470	.....	
SEQ ID NO: 10	IRR RAMDNEWPHVMLFPEGTTTNGKALISFKTGAFSPGLPVQPMVIKYPH	
O35259	.....VHLMCYR.....	
Q9XFJ4	LFGSIDYVSPEALSREKITTKSDIWSLGVILYILLSGYPPFIAPS NRQKQ	
Q24214	.....	300
P28470	.....	
SEQ ID NO: 10	KYVNPCWCNQGGPLVILFQLMTQFVN YMEVEYL PVMT PNVHEIKNPHEFA	
O35259	.....ICVR.....ALTAIITYHNRK	
Q9XFJ4	QMILNGQFSFDEKTWKNISSAKQLISSLKVDPNMRPTAQEILEHPWVT	

29/37

	301	350
Q24214	.....	MGNETSLPME
P28470	.....	GNEASYHSE
SEQ ID NO: 10	NRVRTEMAKALGVVCTEHNF...LDIQLKMAAEKLQPSGRSLVEFARME	
O35259	NRPR.....N.....	GGICVANHT
Q9XFJ4	GDLAKQEQM岱EIVSRLQSFNARRKFRAAAMASILSSSFLRTKLLKKLV	
	351	400
Q24214	MCSNFDADAEIRRLGKRFKLDLD..NSGALSVDEFMSLPELQ.QNPLVQR	
P28470	MGTHFDHDEIKRLGRSFKKMDLD..KSGSLSVDEFMSLPELQ.QNPLVGR	
SEQ ID NO: 10	KLFRLDYSKAQEYLEKFSAMDPS..HSGYVTYDEFLKALHLP.PTQITEQ	
O35259	SRIDVIIFASDGGYYAMVGQVHGG..LMGVIQRAMVKACPHVW.FERSEVK	
Q9XFJ4	GSYDLKPEELENLSHNFKICKNGENSTLEFEELKAMEMSSLVPLAPR	
	401	450
Q24214	VIDIFDADGNGEVDFKEFIQGVSQFS.VKGDKLSKLRFAFRIYDMDNDGY	
P28470	VIDIFDTDGNGEVDFREFIVGTSQFS.VKGDEEQKLRFATRIYDMDNDGF	
SEQ ID NO: 10	VFNLFDKNGHGSINFREFVAGLAFLS.THTSFQTTMKAASFKACDVGDGDT	
O35259	DRHLVAKRLTEHVQDKSKLPILIFPEGTCINNTSVMMFKKGSFEIGATVY	
Q9XFJ4	IFDLFDNNRDGTVDMREIIGGFSSLK..YSQGDDALRLCFQVYDTRSGC	
	451	500
Q24214	ISNGELFQVLKMMVGNNLKD.TQLQQIVDKTIGFADKDEDGKISFDEFCS	
P28470	ISNGELFQVLKMMVGNNLKD.WQLQQLVDKSILVLDKDGDRISFEEFRD	
SEQ ID NO: 10	LTRNEVESSLMAVFP.....ELPPATVLKLFDTLDLNRDGSINWEEFSS	
O35259	PVAIKYDPQFGDAFWN.....SSKYGMVTYLLRMMTSWAIIVCS	
Q9XFJ4	ISKEEVESMLRALPEDCLPINITEPGKLDEIFDLM DANSDGKVTFDEFKA	
	501	532
Q24214	VVGNTDIHKKMVVDV.....	
P28470	VVRTMEIHKKLJVVFDHGQED.....	
SEQ ID NO: 10	FLQRNPEYLAIIIAAHPTLLQAPKSESESETNI	
O35259	VWYLPPTREKDEDAVQFANRVKSAIARQEDW	
Q9XFJ4	AMQRDSSLQDVVLSSLRPN.....	

30/37

Figure 20: Alignment of SEQ ID NO: 12 with Swiss Prot database

1	50
Q9XFW4	.MAMAAAIVPLGILFFISGLVVNLLQAVCYVLVRPM SKNTYRKINRVVA
Q9SDN3	.....
Q40119	MAIPAAAFIVPISLLFFMSGLVVNFIQAVFYVLVRPISKDTYRRINTLVA
Q41745	MAIPLVLVVLPLGLLFLSGLIVNAIQAVLFVTIRPFSKSFYRRINRFLA
Q9SYC8	MKIPAAALVFIPVGVLFLISGLIVNIIQLVFFIIVRPPFSRSLYRRINKVA
SEQ ID NO: 12	.....MIMM
51	100
Q9XFW4	ETLWLELVWIVDWWAGVKIQVFADDETFRNRMGKEHALVV CNHRS DIDWLV
Q9SDN3	.....MGKEHALVVISNHRSDIDWLV
Q40119	ELLWLELVWVIDWWAGVKVQLYTDTESFRLMGKEHALLICNHRSDIDWLI
Q41745	ELLWLQLVWVVDWWAGVKVQLHADEETYRSMGKEHALIIISNHRSDIDWLI
Q9SYC8	ELLWLQLIWLFDWWACIKINLYVDAETLELIGKEHALVLSNHRSDIDWLI
SEQ ID NO: 12	EVLWSELIWLLDWWANVKVKVYTPKESWEHLGKEHALLICNHRSDIDWLV
101	150
Q9XFW4	GWILAQRSGCLGSALAVMKSSKFLPVIGWSMW FSEYLFLERNWAKDEST
Q9SDN3	GWVLAQRSGCLGSSLAVMKSSKFLPVIGWSMW FSEYLFLERSWAKDEGT
Q40119	GWVLAQRCGCLSSSIAVMKSSKFLPVIGWSMW FSEYLFLERNWAKDENT
Q41745	GWILAQRSGCLGSTLAVMKSSKFLPVIGWSMW FAEYLFLERSWAKDEKT
Q9SYC8	GWVMAQRVGCLGSSLAIMKKEAKYLPIIGWSMW FSDYIFLERSWAKDENT
SEQ ID NO: 12	GWIIAQRLGCLGGTRAVMKKSTKFLPVIGWSMW FSEYVFLSRDWAKDEKV
151	200
Q9XFW4	LQSLQRLNDFPRPFWLALFVEGTRFTEAKLKAAQEYAASSELPVPRNVL
Q9SDN3	LKSGVQRLKDFPQ?FWLALFVEGTRFTQAKLLAAQEYAATGLPVPRNVL
Q40119	LKSGLQRLNDFPKPFWLALFVEGTRFTKAKLLAAQEYAASAGLPVPRNVL
Q41745	LKWGLQRLKDFPRPFWLALFVEGTRFTPAKLLAAQEYAASQGLPAPRNVL
Q9SYC8	LKAGFKRLEDFFPMTFWLALFVEGTRFTQEKL EAAQEYASIRSLPSPRNVL
SEQ ID NO: 12	LKNGYSSLKGFPRTLWVALFVEGTRFTKAKLEVAQKFAADTGLRVPRYVL
201	250
Q9XFW4	IPRTKGFVSAVS NMR SFVPAIYDMTVAIPKTSPPPTMLRLFKQPSVHV
Q9SDN3	IPRTKGFVTA VSQMR SFAPAIYDVTVAIPKSSPAPTMRLFEGRPSVHV
Q40119	IPRTKGFVSAVS NMR SFVPAIYDLTVAIPKTT EQPTMLRLFRGKSSVHV
Q41745	IPRTKGFVSAVSIMRDFVPAIYDTTIVPKDSPQPTMLRILKGQSSVIHV
Q9SYC8	IPRTKGFVSAVSEIRSFVPAIYDCTLT VHNQPTPLL RLMFSGQSSEINL
SEQ ID NO: 12	VPRTKGFVSAVENLREFPVVYDMTVAISKE LPNPTMIRIFRGQPSVHV

31/37

	251	300
Q9XFW4	HIKCHSMKDLPEPEDEIAQWCRDQFVAKDALLDKHIAADTFPGQKEQNIG	
Q9SDN3	HIKRHVMRDLPETDEAVAQWCKDIFVAKDALLDKHTVEQTFGDQQLKVTG	
Q40119	HLKRHLMKDLPKTDDGVAQWCKDQFISKDALLDKHVAEDTFSGLEVQDIG	
Q41745	RMKRHAMSEMPKSDEDVSKWCKDIFVAKDALLDKHLATGTFD. EEIRPIG	
Q9SYC8	QMRRHKMSELPETDGGIAQWCQDLFITKDAQLEKYFTKDVFSDLEVHQIN	
SEQ ID NO: 12	YVRRVPMSDLPEGANAISKWCHDAFHDKDRLEQHEKENTFGEDLYIPIE	
	301	350
Q9XFW4	RPIKSLAVVVSWACLLTLGAMKFLHWSNLFSSWKGIALSAFGLGIITLCM	
Q9SDN3	RPLKSLLVVTAWACLLLILGALKFLYWSSLSSWKGIAFSALGLGVVTVLM	
Q40119	RPMKSLVVVVSWMCLLCGLVKFLQWSALLSSWKGMITTFLGIVTVLM	
Q41745	RPVKSLLVTLFWSCLLLFGAIEFFKWTQLLSTWRGVAFTAAGMALVTGVM	
Q9SYC8	RPIKPLIVVIIWLGFUVGGFKLLQWLSIVASWKIILLFVFFLVIATITM	
SEQ ID NO: 12	RPLKPLIIIVISWAITLLAAWWFLRR..VLSTWKGIAWAGVLVVVMLCV	
	351	391
Q9XFW4	QILIRSSQSERSTPAKVAPAKPKDNHQSGPSSQTEVEEKQK	
Q9SDN3	QILIRFSQSERSTPAPVAPTNKNKGESSGKPEKQQ.....	
Q40119	HILIRSSQSEHSTPAKTRARQTAENPK.....	
Q41745	HVFIGMSQAERSSSARAARNRVKKE.....	
Q9SYC8	QILIQSSESQRSTPAKRPLQEQLISA.....	
SEQ ID NO: 12	QILVMSSQSERSSDPAAKKANQKQAAVAHLGKT.....	

**A** Western blot analyses of the *Thraustochytrium* LPAAT expressed in *E. coli* as fusion protein (LPAAT-FP) with N-terminal GST tag and C-terminal His tag.

**B** Acyl-CoA specificity of the *Thraustochytrium* LPAAT expressed as GST fusion protein in *E. coli*

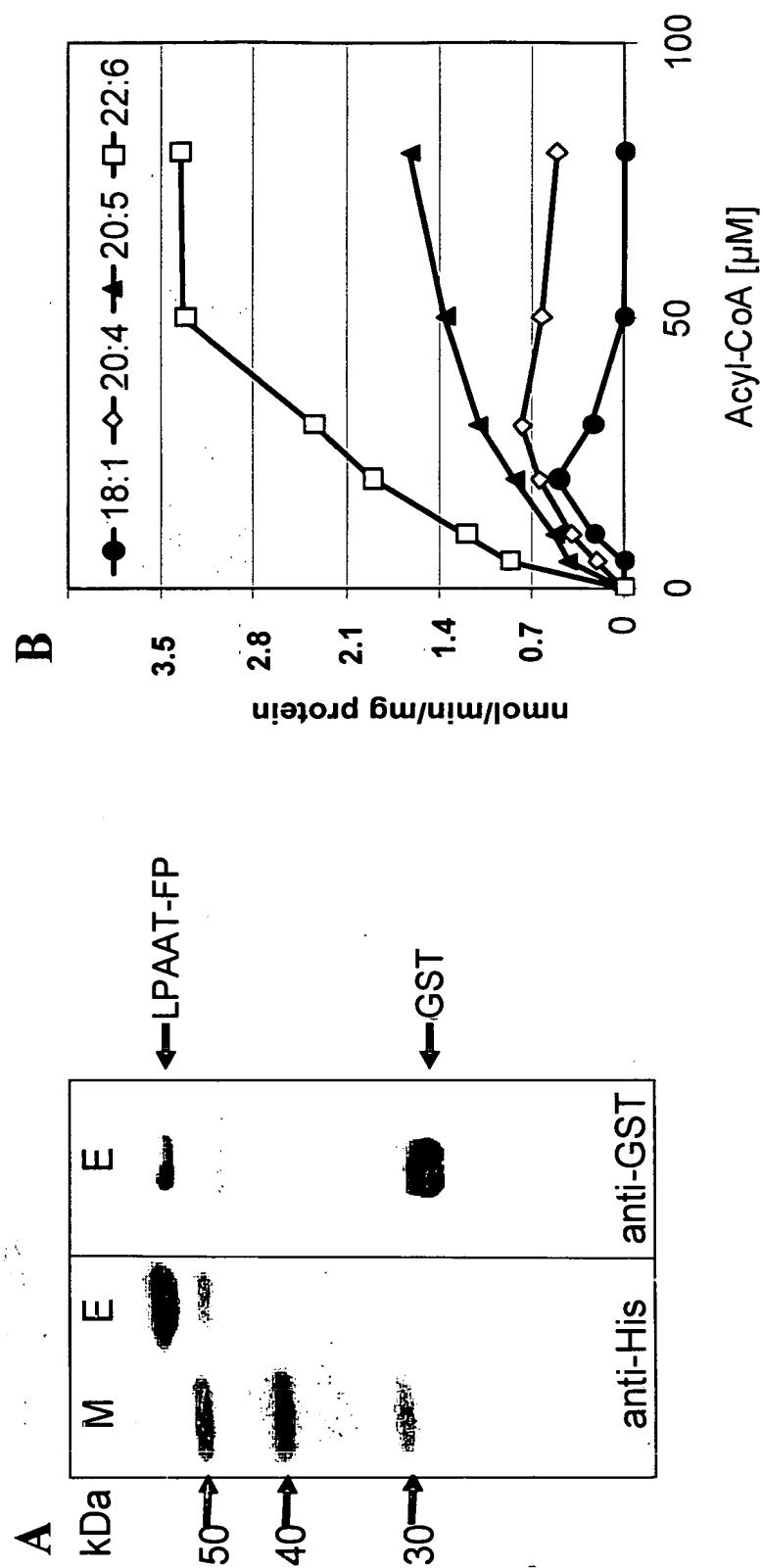


Figure 22: **A:** Western blot analysis of the *Shewanella* LPAAT expressed in *E. coli* as fusion protein with C-terminal His tag.  
**B:** Functional expression of the *Shewanella* LPAAT in *E. coli*

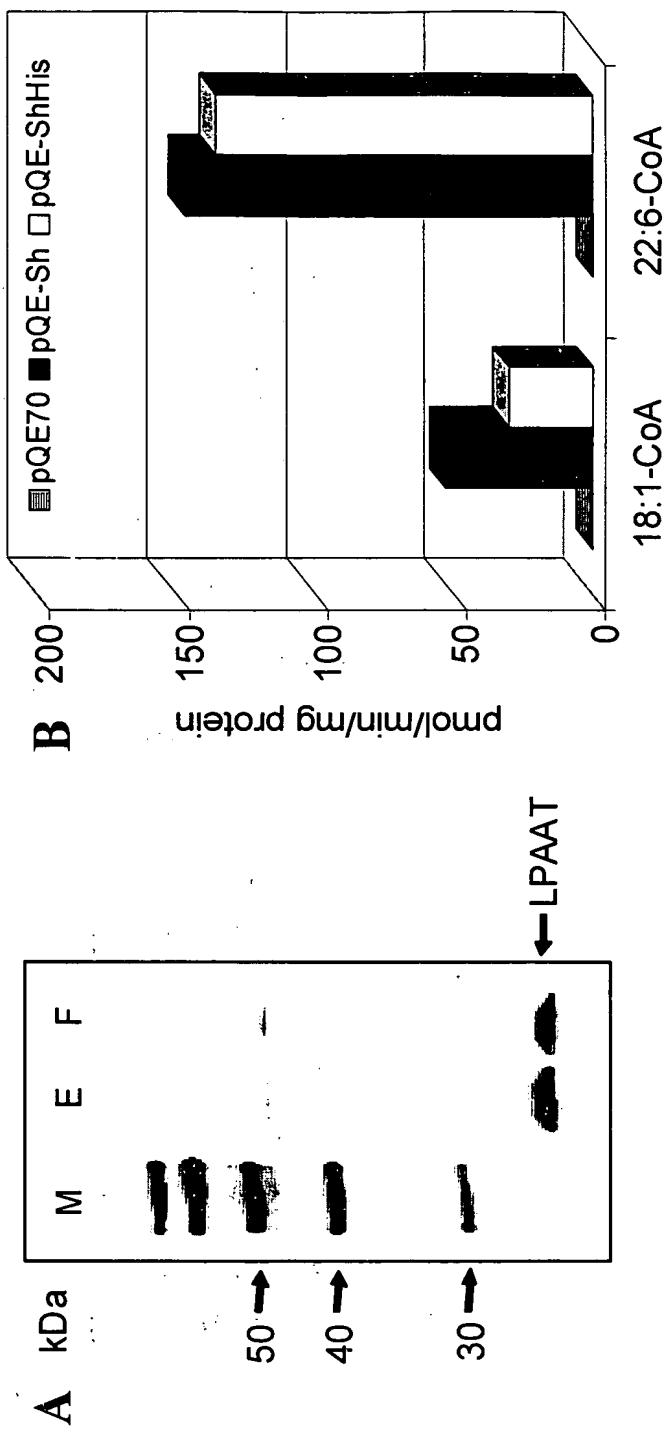


Figure 23: Expression of Mortierella LPAAT (MaB4\_AT) in yeast, and feeding of 18:2  $\Delta$ 9,12 fatty acids (A + B)

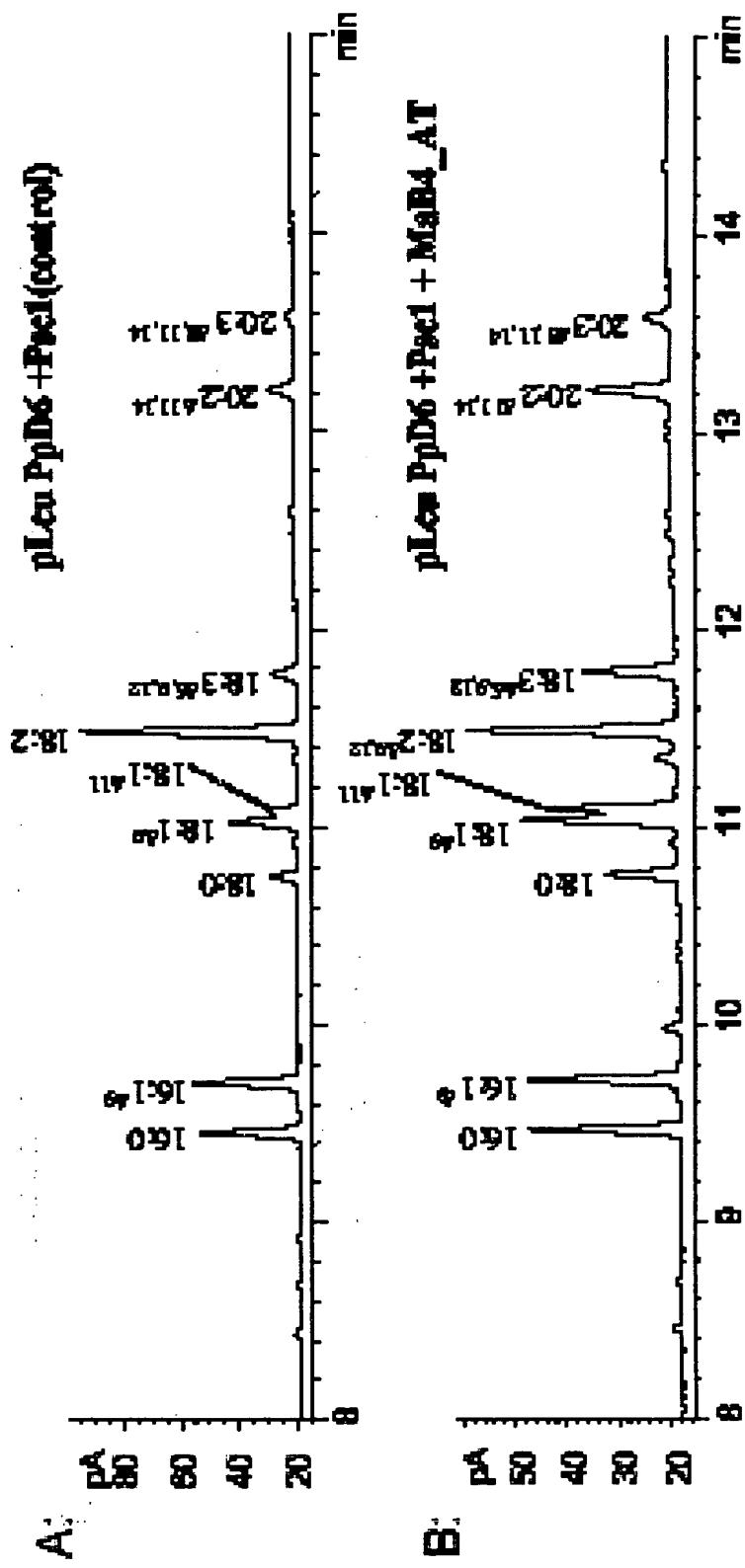


Figure 24: Expression of Mortierella LPAAT (*MaB4\_AT*) in yeast, and feeding of 18:3  $\Delta$ 9,12,15 fatty acids (C + D)

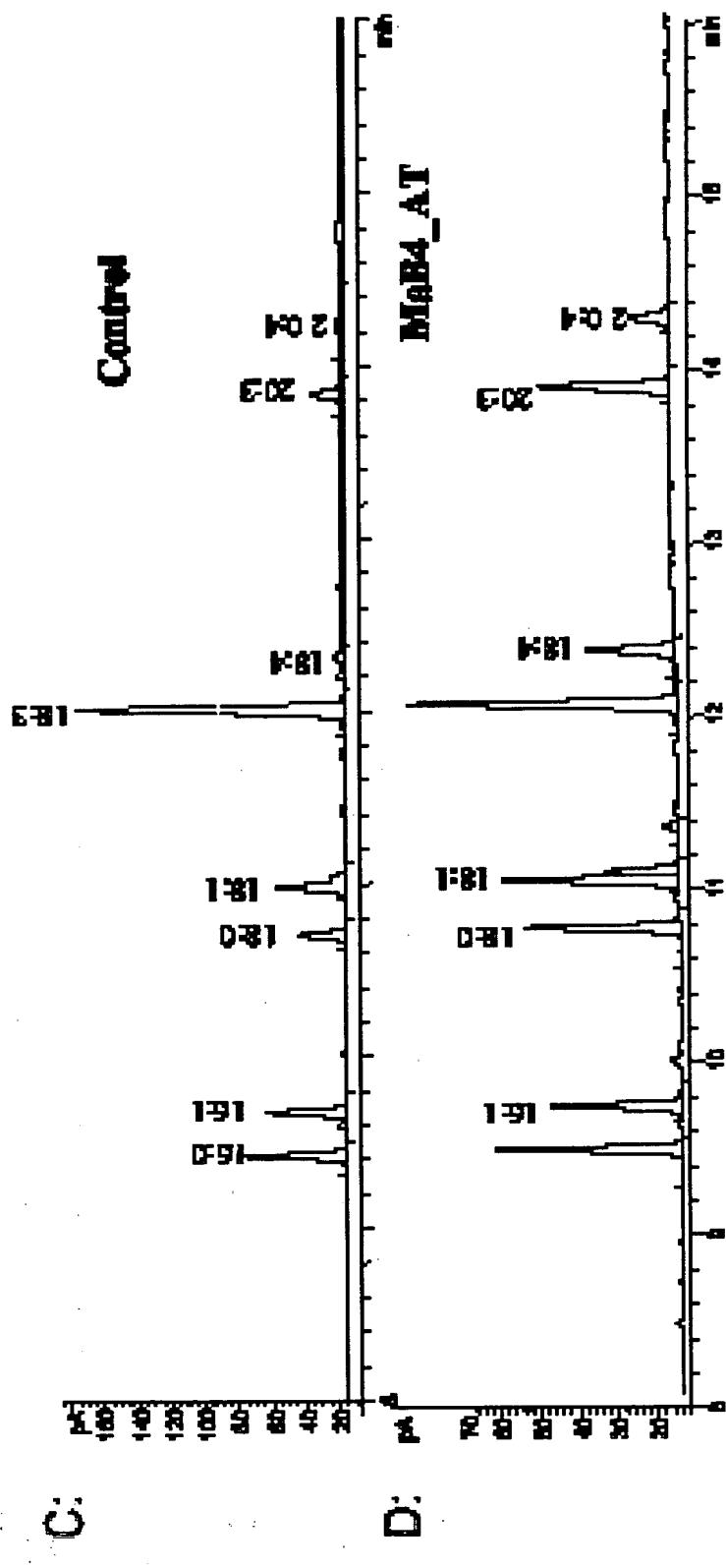
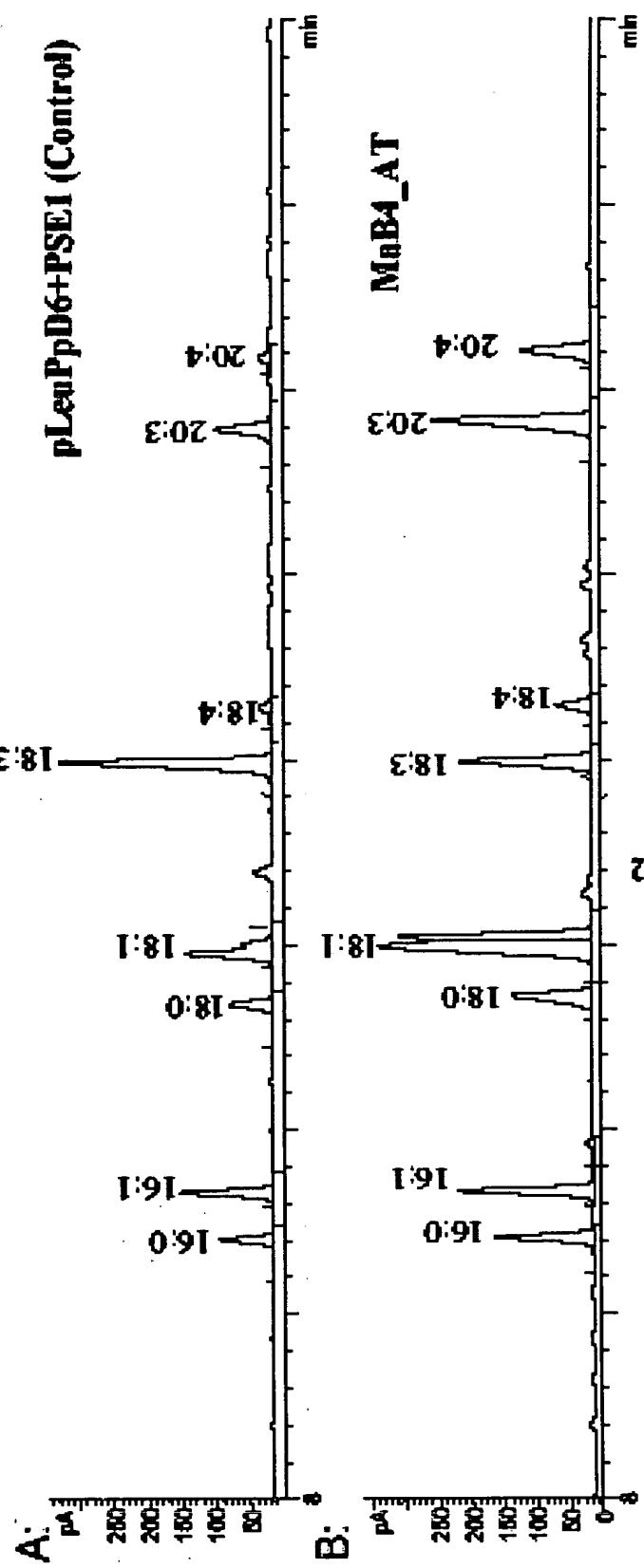
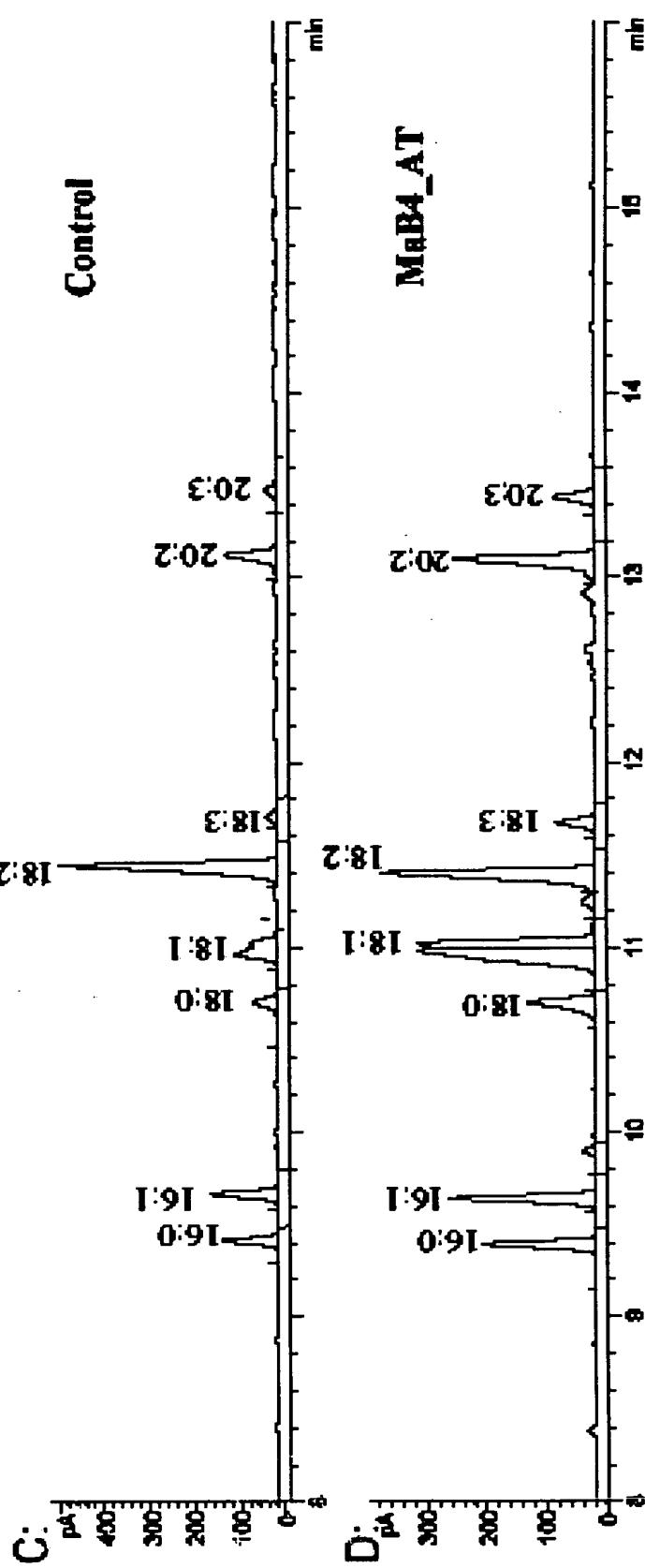


Figure 25: Expression of Mortierella LPAAT (*Mab4\_AT*) in yeast, and feeding of 18:2  $\Delta$ 9,12 fatty acids (A + B). Analysis of the neutral lipids.



37/37

Figure 26: Expression of Mortierella LPAAT (Mab4\_AT) in yeast, and feeding of 18:3 Δ9,12,15 fatty acids (C + D). Analysis of the neutral lipids.



This Page is inserted by IFW Indexing and Scanning  
Operations and is not part of the Official Record

## BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- BLACK BORDERS
- IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT OR DRAWING
- BLURED OR ILLEGIBLE TEXT OR DRAWING
- SKEWED/SLANTED IMAGES
- COLORED OR BLACK AND WHITE PHOTOGRAPHS
- GRAY SCALE DOCUMENTS
- LINES OR MARKS ON ORIGINAL DOCUMENT
- REPERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- OTHER: \_\_\_\_\_

**IMAGES ARE BEST AVAILABLE COPY.**  
**As rescanning documents *will not* correct images**  
**problems checked, please do not report the**  
**problems to the IFW Image Problem Mailbox**